

GenCore version 5.1.6
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Run on: November 17, 2004, 09:57:30 ; Search time 7349 Seconds
 (without alignments)
 11402.551 Million cell updates/see

Title: US-10-009-570-1
 Perfect score: 1772
 Sequence: 1 acttttagataataaggtaag.ctctttctccatgtcaag 1772

Scoring table: IDENTITY_NUC
 Scoring table: Gapop 10_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Commentaire : **Commentaire :**

ALIGNMENTS

RESULT 1
 AX063520
 LOCUS
 AX063520
 DEFINITION Sequence 1 from Patent WO0078975.
 ACCESSION AX063520
 VERSION AX063520.1 GI:12541259

SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	artificial sequences.		
AUTHORS	Donaldson, I.A. and Rasmussen, T.B.		
TITLE	Rice sucrose synthase promoter		
JOURNAL	WO 0078975-A1 28-DEC-2000;		
DANISCO (DK)			Location/Qualifiers
FEATURES			

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Db	181	CACTGGCAGGGCATGCACTTGGTCCGGACATGGAGGTGTGGCAGATGGACAGGTAC	240					

SMARTFC

sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs representing the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level (such as same name, 'putative', and '-like protein'). A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a 'probable', 'hypothetical', protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from M13rev to -21M13 of the BAC clone. This sequence of B1056G08 clone has an overlap with p01616_D06 (DDBJ: AP005198) at 5', end and an overlap with P0552F09 clone (DDBJ: AP013308) at 3', end and an overlap with P050B08 clone (DDBJ: AP004909) at 3', end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dnaaffrc.go.jp/GenomeSeq.html>. <http://rgp.dnaaffrc.go.jp/GenomeSeq.html>

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CDS

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RESULT 4

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ORGANISM	Oryza sativa				
REFERENCE					
AUTHORS	Chang, H. S., Chen, W., Cooper, B., Glazebrook, J., Goff, S. A., Hou, Y. M., Katagiri, F., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.				
TITLE	Plant genes involved in defense against pathogens				
JOURNAL	Plant: WO 03000898-A 6515 03-JAN-2003;				
FEATURES	syngenta Participations AG (CH)				
ORIGIN	1. 2000 /organism="Oryza sativa" /mol_type="unassigned DNA" /db_xref="taxon:4530"				
Query Match	Score 1082.4; DB 6; Length 2000;				
Best Local Similarity	99.3%; Pred. No. 1.7e-253;				
Matches 1098; Conservative	0; Mismatches 6; Indels 2; Gaps 1;				
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Db	1 CGCTTAATGCTGAGATAAAATTCTATAGATCATTATAAATCATTTAGTTAGTGTCT 60				
Qy	729 TCGTCATTTCTTCACTATCAACCATAGCTCAACTGTCATAATGACATAAAGTT 788				RESULT 6
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Qy	789 ACTAACGACATCGCTCATCACACCCAAAGCTCACGGTGGTGCCTCAGACAGA 848				LOCUS
Db	121 ACTAACGACATCGCTCATCACACCCAAAGCTCACGGTGGTGCCTCAGACAGA 180				AP005890
Qy	849 GTTTAGCACTTGTGCAACATATATGCTGCGATGACATCTACTGATGCGCATGCGAAT 908				DEFINITION
Db	181 GTTTAGCACTTGTGCAACATATATGTTGCAATCATCTACTGATGCGCATGCGAAT 240				*** SEQUENCING IN PROGRESS ***.
Qy	909 TTTAGGGTTCTTCACTGCGTTTCAACGGGACAGGGCTGAGCAGCAGTTCATGCGAT 968				ACCESSION
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Qy	969 GGCTCCTGTAAAAACAAAAAGGTACTGGTAATACTGCTGTAGTAGTTAGCA 1028				KEYWORDS
Db	301 GGCTCCTGTAAAAACAAAAAGGTACTGGTAATACTGCTGTAGTAGTTAGCA 360				HTGS PHASE2.
Qy	1029 GAATGCGAAGGCCATGCTATGCAATGCTATGCAAGTATGCTGTAGTTAGCT 1088				Orzya sativa (japonica cultivar-group)
Db	361 GAATGCGAAGGCCATGCTATGCAATGCTATGCAAGTATGCTGTAGTTAGCT 420				Orzya sativa (japonica cultivar-group)
Qy	1089 AGCCAGCTAACTAATCATGCGAGGCCAGCAAGCTCCCATGCTGTAGTTAGCA 1148				Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Db	481 CTCCAGTAATCTAGTGTAAATTCTACCGAACTTACCTGCGATGCTGTAGTTAGCA 540				1. Sasaki, T., Matsumoto, T. and Katayose, Y.
Qy	1209 ATATTACCAAGGTTACAATCCCGTTACCTGCGAAATCTACCTGCGATGCTGTAGTTAGCA 1268				Published Only in Database (2002)
Db	541 ATATTACCAAGGTTACAATCCCGTTACCTGCGAAATCTACCTGCGATGCTGTAGTTAGCA 600				Sasaki, T., Matsumoto, T. and Katayose, Y.
Qy	1269 GTTTTCGTTAAACCGCTGTTAACCGCAAAATAGACAATTTGCAAAATTAA 1328				Direct Submission
Db	601 GTTTTCGTTAAACCGCTGTTAACCGCAAAATAGACAATTTGCAAAATTAA 660				JOURNAL
Qy	1329 ATTTTGTAGTTTAACTGCTGTTAACCTAGCCGGAAACCTTGAGTTGTGTGTCAGCTGT 1386				COMMENT
Db	661 ATTTTGTAGTTTAACTGCTGTTAACCTAGCCGGAAACCTTGAGTTGTGTGTCAGCTGT 720				NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
Qy					* NOTE: This is a 'working draft' sequence.
Db					* This sequence will be replaced
Qy					* by the finished sequence as soon as it is available and
Db					* the accession number will be preserved.
Qy					LOCATION/Qualifiers
Db					1. 139653
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Db					/mol_type="genomic DNA"
Qy					/cultEivar="Nipponbare"
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Db					/clonename="IRI09qC06"
FEATURES					
source					

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RESULT 7				/note="TNF2-like protein"
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LCUS	Oryza sativa (japonica cultivar-group)	genomic DNA, chromosome 9,		/gene="OSUNBA0064I23..2..2"
DEFINITION	ORCA clone:OSUNBA0064I23.			complement (join(<3012..3105,3133..4458))
ACCESSION	AP005912			/gene="OSUNBA0064I23..2..2"
VERSION	AP005912..3	GI:51091694		/note="supported by full-length cDNA(s): AK065973"
KEYWORDS				complement (3022..5151)
SOURCE	Oryza sativa (japonica cultivar-group)			/gene="OSUNBA0064I23..2..1"
ORGANISM	Oryza sativa (japonica cultivar-group)			complement (<3022..>5151)
VERSION	Oryza sativa Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhrhartoideae; Oryzeae; Oryza.			/gene="OSUNBA0064I23..1..1"
REFERENCE	Sasaki, T., Matsumoto, T. and Katayose, Y.			/note="supported by full-length cDNA(s): AK065973"
AUTHORS				complement (join(3022..3105,3133..4423))
TITLE	Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC clones:OSUNBA0064I23			/gene="OSUNBA0064I23..2..2"
JOURNAL	Published Only in Database (2002)			/note="TRIM2 protein-like"
REFERENCE	2 (bases 1 to 161865)			complement (join(3101..3105,3133..4423))
AUTHORS	Sasaki, T., Matsumoto, T. and Katayose, Y.			/gene="OSUNBA0064I23..1..1"
TITLE	Direct Submission			join(7380..7421,7917..8131,9249..9289,10326..11191)
JOURNAL	Submitted (1-NOV-2002) Takaji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8002, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)			join(7380..7421,7917..8131,9249..9289,10326..11191)
COMMENT	On Aug 9, 2004 this sequence version replaced Gi:46092394. Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://www.tigr.org/tdb/glimmer/glimmer.html), RiceHMM (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bioinformatics.iastate.edu/cgi-bin/sp_cgi/), S1m4 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (http://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologs of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs representing the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs representing the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no.			
	A Gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, putative- and -like protein. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.			
	The orientation of the sequence is from -21M13 to M13rev of the BAC clone. This sequence of OSUNBA0064I23 clone has an overlap with OSUNBB0079K11 (DDBJ: AP005971) clone at 5' end and an overlap with			
				/note="similar to Oryza sativa chromosome 10."

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gene	complement (27032..29638)	61 AGACAGTGTGTCAACAGTACAAGTAAACTCAAAATCCTTATAATTGGAC 115
mRNA	complement (join(<27032..27136,27374..27487,27598..28519, 29911..>29638))	62 AGACAGTGTGTCAACAGTACAAGTAAACTCAAAATCCTTATAATTGGAC 106806
	/gene="OSJNBA0064123_8" /note="start and end point are not identified" complement (join(27032..27136,27374..27487,27598..28519, 29691..29698))	RESULT 8 OSJN00076/C
CDS	/gene="OSJNBA0064123..8" /codon_start=1 /product="cell wall protein-like" /protein_id="BAD36497_1" /db_xref="GI:51091696"	LOCUS OSJN00076/C 173770 bp DNA linear PLN 10-FEB-2004 DEFINITION Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBA0039K24, complete sequence.
	/translation="MTTRPCCRVTTPGAVASSSSAASSSSPAYPPBPAETSGASP PATVVLPPRERLPPRPLSPRPRCGRPRHLSRHSRASVLSPGATVSPFRRNAVISA SPFSSAPPSSARRPAAPPSPSQRERPRRFLVSDRERRRERGRPAR RLAAPPSSRRLRVRPVRPRAAAAGCPRLAAGPERRRRCRPLVYPPGRDVRPSV PFSEFVYRVOASCSPVLEFLVLAASSSSPPAASLRSIAKEVPSVSAAAPVRC RSHASSEGGKSRCPVLSVCPVLSVCPVLSVCPVLSVCPVLSVCPVLSVCPVLSV CVLGLPSPFRLTGACSFVLRVAFVYVPEPEAWFAVARESEGSL"	ACCESSION AL606637..3 VERSION GI:32480037 KEYWORDS HTG, SOURCE (Japonica cultivar-group) ORGANISM Oryza sativa (Japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhrhartooideae; Oryzeae; Oryza.
gene	/gene="OSJNBA0064123..9" /note="start and end point are not identified" join(<31219..31224,31470..31494,31821..31985)	1 Feng, Q., Zhang, Y., Hao, P., Wang, S., Fu, G., Huang, Y., Li, Y., Zhu, J., Liu, Y., Hu, X., Jia, P., Zhang, Y., Zhao, Q., Ying, K., Yu, S., Tang, Y., Weng, Q., Zhang, L., Lu, Y., Mu, J., Lu, Y., Zhang, L.S., Yu, Z., Fan, D., Liu, X., Lu, T., Li, C., Wu, Y., Sun, T., Lei, H., Li, T., Hu, H., Guan, J., Wu, M., Zhang, R., Zhou, B., Chen, Z., Wang, Z., Guan, J., Yin, H., Cai, Z., Ren, S., Lv, G., Gu, W., Zhu, G., Tu, Y., Jia, J., Zhang, Y., Chen, J., Kang, H., Wang, L., Chen, X., Shao, C., Sun, Y., Hu, Q., Zhang, X., Zhang, W., Wang, L., Ding, C., Sheng, H., Gu, J., Chen, S., Ni, L., Zhu, F., Chen, W., Lan, L., Lai, Y., Cheng, Z., Gu, M., Jiang, J., Li, J., Hong, G., Xue, Y., and Han, B.
mRNA	/codon_start=1 /product="U1P1 protease-like protein" /protein_id="BAD36498_1" /db_xref="GI:51091697"	TITLE Sequence and analysis of rice chromosome 4 JOURNAL Nature 420 (6913), 316-320 (2002) PUBMED 22331377 REFERENCE 2 AUTHORS Feng, Q., Huang, Y.C., Li, Y., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Weng, Q.J., Zhang, L., Liu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, C., Liu, T., Zhang, Y., Hu, H., Jia, P.X., Qian, Y.M., Ying, K., Zhou, B., Chen, Z.H., Hao, P., Zhang, L., Wu, M., Zhang, R., Qian, J.P., Guan, J.P., Wang, S.Y., Ren, S.X., Lv, G., Lin, W., Gu, W.Q., Zhu, G.F., Tu, Y.F., Jia, J., Yin, H.P., Zhang, Y., Cai, Z., Chen, J., Kang, H., Chen, X.Y., Shao, C.Y., Sun, Y., Hu, Q.P., Zhang, X.L., Zhang, W., Wang, L.J., Ding, C.W., Sheng, H.H., Gu, J.L., Chen, S.T., Ni, L., Zhou, F.H., and Hong, G.P.
	/translation="MGGRYQKQKMDRMISNYKATRYRHFVTFKQLSTRVGGVRCHIENNLKCRV VAPNLPIKDNLSHSTGHWTQVYK"	Direct Submission Submitted (08-SEP-2001) Han Bin, National Center for Gene Research, Chinese Academy of Sciences, 500# Cao Bao Road, Shanghai 200233, CHINA. E-mail enquiries: bhan@ncgr.ac.cn clone: OSJNBA0039K24.
gene	/gene="OSJNBA0064123..10" /note="start and end point are not identified" complement (join(33472..33554,34461..34876..>34921))	TITLE ORyza sativa (nippobare) genomic DNA, chromosome 4, BAC JOURNAL COMMENT On Jul 8, 2003 this sequence version replaced gi:21912475. REMARK Web site: http://www.ncbi.ac.cn bhan@ncgr.ac.cn COMMENT Web site: http://www.ncbi.ac.cn ----- Summary Statistics Assembly program: phrap
mRNA	/gene="OSJNBA0064123..10" /note="start and end point are not identified" complement (join(33472..33554,34461..34876..>34921))	This is a complete sequence. Genes were identified by a combination of several methods: Gene genescan (http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHM (http://genemark.biology.gatech.edu/GeneMark/), tRNACan-SE (Sean complete sequence against NCBI tRNAscan-SE), searches of the (ftp://nobii.nim.nih.gov/blast/db) and the EST database at NGR. Location.Qualifiers
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gene	/gene="OSJNBA0064123..11" /note="start and end point are not identified" join(36149..36529,36823..37200)	FEATURES Source 1..173770
mRNA	/gene="OSJNBA0064123..11" /note="start and end point are not identified" join(36149..36529,36823..37200)	Query Match

卷之三

Query Match 5.6%; Score 99.8; DB 8; Length 173770;
 Best Local Similarity 79.8%; Pred. No. 2e-13;
 Matches 130; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

Qy	1	ACTTGTAGATATAAGTAAAGTCACAGAAAATAATAATTCCAAATTTTTAATA	60	RESULT 10
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Qy	61	AGACGAGTGGTCAAACAGTCAAGTAAACTCAAATCTTATATTGGGAC-TTAT	119	AC090485/1
Db	17153	AGACGAGTGGTCAAACAGTCAAGTAAACTCAAATCTTATATTGGGAC-TTAT	17094	AC090485/1
Qy	120	ATTATGGACGGGAGGAACTTGAAGATTTGACCAAGAAA 162	17093	AC090485/3
Db	17093	ATTATGGACGGGAGGAACTTGAAGATTTGACCAAGAAA 17051	17051	GI:14495164
RESULT 9				
AC145780	AC145780	88044 bp DNA linear PLN 31-JUL-2004		
LOCUS		Oryza sativa chromosome 3 BAC clone OSJNBB0069P02, complete		REFERENCE 1
DEFINITION		sequence.		AUTHORS de la Bastide,M., Spiegel,L., Preston,R., Kirchoff,K., King,L.,
ACCESSION	AC145780			Nascimanto,L., Baker,J., Vil,M.D., Zutavern,T., Santos,L.,
KEYWORDS	HTG.	GI:50872484		Miller,B., Kuit,K., Cunnis,D.M., Rodriguez,S., Balija,V., Shah,R.,
SOURCE	Oryza sativa (japonica cultivar-group)			Bahret,A., Yang,C., Bell,M., Palmer,L., O'Shaughnessy,A., Dedhia,N.,
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae;			and McCombie,W.R.
REFERENCE	1 (bases 1 to 88044)			Genomic Sequence for Oryza sativa, Nipponbare strain, clone
AUTHORS	Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M.,			OSJNBB0069N01, From chromosome 3, complete sequence
TITLE	Taiwan,I.L., Tsitman,T., Kim,M., Bera,J., Jin,S., Padrosh,D.W.,			Unpublished
JOURNAL	Tallion,L., Koo,H., Zisman,M., Hsiao,J., Blunt,S., Vanaken,S.,			2 (bases 1 to 159636)
REFERENCE	Riedmuller,S.B., Utterbach,T., Feldblyum,T., Yang,Q., Haas,B.,			McCombie,W.R.
AUTHORS	Suh,B., Peterson,J., Quackenbush,J., White,O., Saizberg,S., and			Direct Submission
TITLE	Fraser,C.			Submitted (20-JUN-2001) Lita Annenberg Hazen Genome Center, Cold
JOURNAL	Oryza sativa ssp. japonica cv. Nipponbare OSJNBB0069P02 BAC genomic			Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor,
REFERENCE	2 (bases 1 to 88044)			NY 11724, USA
AUTHORS	Buell,R.			4 (bases 1 to 159636)
TITLE	Unpublished			Palmer,L.E., de la Bastide,M., Spiegel,L., Preston,R., Kirchoff,K.,
JOURNAL	Direct Submission			King,L., Nascimanto,L., Baker,J., Vil,M.D., Zutavern,T., Santos,L.,
REFERENCE	Submitted (26-JUL-2003) The Institute for Genomic Research, 9712			Miller,B., Kuit,K., Cunnis,D.M., Rodriguez,S., Balija,V., Shah,R.,
AUTHORS	3 (bases 1 to 88044)			Bahret,A., Yang,C., Bell,M., O'Shaughnessy,A., Dedhia,N., and
TITLE	Buell,R.			McCombie,W.R.
JOURNAL	Direct Submission			Direct Submission
COMMENT	Submitted (31-JUL-2004) The Institute for Genomic Research, 9712			Submitted (06-SEP-2001) Lita Annenberg Hazen Genome Center, Cold
FEATURES	On Jul 31, 2004 this sequence version replaced gi:33285037.			Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY
source	1. 88044			11724, USA
ORIGIN	/organism="Oryza sativa (japonica cultivar-group)"			Genomic Sequence for Oryza sativa, Nipponbare strain, clone
	/mol_type="genomic DNA"			OSJNBB0069N01, From chromosome 3, complete sequence
	/cultivar="Nipponbare"			On Jun 20, 2001 this sequence version replaced gi:14209722
	/db_xref="taxon:39947"			This sequence was finished as follows unless otherwise noted: all
	/chromosome="3"			regions were either double-stranded or sequenced with an alternate
	/clone="OSJNBB0069P02"			chemistry or covered by high quality data (i.e., phred quality >=
	/note="japonica cultivar-group"			30); an attempt was made to resolve all sequencing problems, such
				as compressions and repeats; all regions were covered by at least
				one plasmid subclone or more than one M13 subclone; and the
				assembly was confirmed by restriction digest.
			Location/Qualifiers	
			1. 159636	/organism="Oryza sativa (japonica cultivar-group)"
				/mol_type="genomic DNA"
				/cultivar="Nipponbare"
				/db_xref="taxon:39947"
				/chromosome="3"
				/clone="OSJNBB0067N01"
				/clone lib="HindIII"
				repeat_region complement (85..91)
				gene 1532..2626
				/gene="transposon02 TNP2-like transposon protein gi 4"
				/note="Hypothetical protein"
				1532..2626
				/gene="OSJNBB0067N01.1"
				CDS /note="Similar to Pir T46123 hypothetical protein"

T2013.90 - Arabidopsis thaliana Identities = 119/339

Evaluate= 3e-44"

/codon_start=1

/product="Hypothetical protein"

/protein_id="AAK98722_1"

/db_xref="GI: 15451598"

/translation="MIDAVHEPKVKWVAPSSSDFREEYTSAAFFESTYNDWARVLDT
LAQAAALIVPRHGGCAASKRLPSYRFAEHJLEPDORAAVAAALASPRGSRLPDPVR
QPFALLAASQRLREVOQSSGDLRGLDAGRHRHTRSVARLRLAUSVPTAVAV
VAVYAGCISVHILAAFAAPMMSPAWLGFRFSGRRABALVOLEAAAKGTYLNRDM
ETISLVLARVTRDEGHMVALRQLRGEAGGKGRLVQEVRQLSKNESESFRQQL
DELEBHLFLCUMTINKARIMMNFMAAAR"

complement (3166..5556)

/gene="OSUNBa0067N01_2"

/note="Putative signal peptidase"

complement (join(3166..3273, 4313..4387, 5109..5274,

/db_xref="GI: 15451596")

/gene="OSUNBa0067N01_2"

/note="Similar to emb|[CnC09470_1] (AL442113) putative
signal peptidase [Oryza sativa] Identities = 68/138
Evaluate= 7e-33"

/codon_start=1

/product="Putative signal peptidase"

/protein_id="AAK98723_1"

/db_xref="GI: 15451599"

/translation="WENCNICBLLPELGAVVAAEBCS1QKYOFSHGDVYFLKCPSDHRE
LFVKRLLALPEGWMLQPGTDIPIKEPHGWVEGNAACSWDSSSFGEPE'DGIKDSMG
GVRVSSASGMGTPGPPR1PLGHJIKGRVAVHWPSPSKIGRVTDKMPNTRISPL"

/gene="OSUNBa0067N01_3"

/note="Unknown protein with similarity to
methyltransferases and transcriptional regulators"
join(7459..9132, 924..9330, 9641..9745, 9839..9947,
10446..10597, 10718..10855)

/gene="OSUNBa0067N01_3"

/note="Similar to db|[BA85534_1] (AP000969) Similar to
Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
(AL049481) [Oryza sativa] Identities = 571/759 Evaluate= 0.0;
Similar to sp|[F25583] [KAR4 YEAST KARYOGAMY PROTEIN
KAR4] Identities = 98/328 Evaluate= 2e-27"

/codon_start=1

/product="Unknown protein with similarity to
methyltransferases and transcriptional regulators"
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/db_xref="GI: 15451600"

/translation="MDSRSPKSPRSPSPDDSDKDRNDRNDSSRTYGSBT
CKEERCDTNRKGSAMGEDVDDDSRSEVDTETVHNDKODRRAVEIKNLHDVYGO
SDYQEQQLGLNERRNGTVDSDDAHTDKLGSGRDRNWTGKTQPEGSVYLSRCK
DSQNTVDTGTRPQNPTRELLTSVAEDYPLCRELJLORKDIBVAGASAPMNYKCDLR
TRPNNSLDEGRGSUSGRDQGGFHERVGYTRDFGRERSETRGSSSTYGSRDTSDSIE
TRPLSISBFGRKFDVILDPWPEYHWRAPGTDHBYWNSBEILRADMKYLGNLISWSRGSKL
LNGIKGTVRRTDGHVTHANDTDIIADEPTDGSNKKPEMYRILTHEALGKRUEL
EFGEDINIRPGKPKSPPHK"

/note="misc rep03 similar to Rat tandem repeat mRNA"

/note="misc rep03 similar to Rat tandem repeat mRNA"

/note="Gaigin_012 MITE element from gb:U72728 Oryza 1"

/note="Wanderer_OSS MITE element from gb:x13679 Oryza"

/note="Gaigin_012 MITE element from gb:U72728 Oryza 1"

170/488 Evaluate= 3e-59"

/codon_start=1

/product="Putative retroelement"

/protein_id="AAK98725_1"

/db_xref="GI: 15451601"

/translation="M0EG5EVHNRFPNPKMCLDEAEDFSIRVKGTSVHVKVKWTKOEA
EAVGRLHEWWTWVTCGIDPEMDKDYDPIHVGNSNGPVIEYDMVSLKTKVYJRVGMMT
RNKPKRKAFAASSNGVLEKAGDKEKTAUYEEDFSNDAEQLVKKQEDBNEALRQ
QLEQFKQIQDQDVKVQGMIEGGIRAOQAGESENEKPKKTQGMAEDEKKSRLRM
DSEBVYDDEPAFVQLVGEQEBENMSEFQAVGVLQIDEMTEKKKSLRM
EKEDKVKVADAAEKEANAFAINKDCALEAVDTNLNLKNEELARINFLEKQKUNL
KGCECENGINLSNIDINDEVLHSDDCMSDFDYAEMLRLSOSNLSGKCRKRNQNL
EIKVTPKCSGNERKKTKKRS"

21418..24126

/note="Class 6712"

21783..23439

/gene="OSUNBa0067N01_5"

/note="Putative retroelement"

join(21783..22427, 22632..23195, 23365..23439)

/gene="OSUNBa0067N01_5"

/note="Similar to sp|[P11369] POL2_MOUSE RETROVIRUS-RELATED

POL POLYPROTEIN [CONTAINS"

/codon_start=1

/product="Putative retroelement"

/protein_id="AAK98726_1"

/db_xref="GI: 15451602"

/translation="M0NWEQYKRCQKOEUNGKIEDIDKCKCERAYGHTLKERGDKD
LKKVYREDLKKWMCRKBNLLEGDDNTKYYHAKANGRKBNMYSLQDQDGEKGQNS
DLMKYTFNFKYVQVBTFKHFYWLJIKDDMLMEFLGMLKAMKGPDIWCDKQV
NKAPOPDGFFPVBTFKHFYWLJIKDDMLMEFLGMLKAMKGPDIWCDKQV
LHKLIDFKEVDNIMKMSFYKMMKAKGPDIDWCDKQV
LHQJLQDSEYARNLKFMICUFIQOLTGKJLKVNFQKIFSEVCLGEAERQDSYSQFTCQIGRL
PMKTFQGPIQDLEKFLFVFGDPECGKJLKVGNL"

repeat_region

/note="Putative signal peptidase"

/note="Putative Tourist type MITE element"

/note="Tourist03 putative Tourist type MITE element"

/note="Wanderer_Osi MITE element from gb:L28995 Oryza"

/note="Castaway_Os2 MITE element from gb:D26547 Rice"

/note="G340 Oryza sativa repetitive element G340_9i|5"

gene 34133..36012

/gene="OSUNBa0067N01_6"

/note="Putative anion transporter"

join(34133..35347, 35444..35633, 35744..36012)

/gene="OSUNBa0067N01_6"

/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

Evaluate= e-174"

/codon_start=1

/product="Putative anion transporter"

join(34133..35347, 35444..35633, 35744..36012)

/gene="OSUNBa0067N01_6"

/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

Evaluate= e-174"

/codon_start=1

/product="Putative anion transporter"

join(34133..35347, 35444..35633, 35744..36012)

/gene="OSUNBa0067N01_6"

/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

Evaluate= e-174"

/codon_start=1

/product="Putative anion transporter"

join(34133..35347, 35444..35633, 35744..36012)

/gene="OSUNBa0067N01_6"

/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

Evaluate= e-174"

/codon_start=1

/product="Putative anion transporter"

join(34133..35347, 35444..35633, 35744..36012)

/gene="OSUNBa0067N01_6"

/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

Evaluate= e-174"

/codon_start=1

/product="Putative anion transporter"

join(34133..35347, 35444..35633, 35744..36012)

/gene="OSUNBa0067N01_6"

/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

170/488 Evaluate= 3e-59"

/codon_start=1

/product="Putative retroelement"

/protein_id="AAK98725_1"

/db_xref="GI: 15451601"

/translation="M0EG5EVHNRFPNPKMCLDEAEDFSIRVKGTSVHVKVKWTKOEA
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RNKPKRKAFAASSNGVLEKAGDKEKTAUYEEDFSNDAEQLVKKQEDBNEALRQ
QLEQFKQIQDQDVKVQGMIEGGIRAOQAGESENEKPKKTQGMAEDEKKSRLRM
DSEBVYDDEPAFVQLVGEQEBENMSEFQAVGVLQIDEMTEKKKSLRM
EKEDKVKVADAAEKEANAFAINKDCALEAVDTNLNLKNEELARINFLEKQKUNL
KGCECENGINLSNIDINDEVLHSDDCMSDFDYAEMLRLSOSNLSGKCRKRNQNL
EIKVTPKCSGNERKKTKKRS"

21418..24126

/note="Class 6712"

21783..23439

/gene="OSUNBa0067N01_5"

/note="Putative retroelement"

join(21783..22427, 22632..23195, 23365..23439)

/gene="OSUNBa0067N01_5"

/note="Similar to sp|[P11369] POL2_MOUSE RETROVIRUS-RELATED

POL POLYPROTEIN [CONTAINS"

/codon_start=1

/product="Putative retroelement"

/protein_id="AAK98726_1"

/db_xref="GI: 15451602"

/translation="M0NWEQYKRCQKOEUNGKIEDIDKCKCERAYGHTLKERGDKD
LKKVYREDLKKWMCRKBNLLEGDDNTKYYHAKANGRKBNMYSLQDQDGEKGQNS
DLMKYTFNFKYVQVBTFKHFYWLJIKDDMLMEFLGMLKAMKGPDIWCDKQV
NKAPOPDGFFPVBTFKHFYWLJIKDDMLMEFLGMLKAMKGPDIWCDKQV
LHKLIDFKEVDNIMKMSFYKMMKAKGPDIDWCDKQV
LHQJLQDSEYARNLKFMICUFIQOLTGKJLKVGNL"

repeat_region

/note="Putative signal peptidase"

/note="Putative Tourist type MITE element"

/note="Tourist03 putative Tourist type MITE element"

/note="Wanderer_Osi MITE element from gb:L28995 Oryza"

/note="Castaway_Os2 MITE element from gb:D26547 Rice"

/note="G340 Oryza sativa repetitive element G340_9i|5"

gene 34133..36012

/gene="OSUNBa0067N01_6"

/note="Putative anion transporter"

join(34133..35347, 35444..35633, 35744..36012)

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/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

Evaluate= e-174"

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/product="Putative anion transporter"

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/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

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/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

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/product="Putative anion transporter"

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/gene="OSUNBa0067N01_6"

/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

Evaluate= e-174"

/codon_start=1

/product="Putative anion transporter"

join(34133..35347, 35444..35633, 35744..36012)

/gene="OSUNBa0067N01_6"

/note="Similar to gb|[AAC24385..1] (U89959) Hypothetical

protein [Arabidopsis thaliana] Identities = 333/556

170/488 Evaluate= 3e-59"

/codon_start=1

/product="Putative retroelement"

/protein_id="AAK98725_1"

/db_xref="GI: 15451601"

/translation="M0EG5EVHNRFPNPKMCLDEAEDFSIRVKGTSVHVKVKWTKOEA
EAVGRLHEWWTWVTCGIDPEMDKDYDPIHVGNSNGPVIEYDMVSLKTKVYJRVGMMT
RNKPKRKAFAASSNGVLEKAGDKEKTAUYEEDFSNDAEQLVKKQEDBNEALRQ
QLEQFKQIQDQDVKVQGMIEGGIRAOQAGESENEKPKKTQGMAEDEKKSRLRM
DSEBVYDDEPAFVQLVGEQEBENMSEFQAVGVLQIDEMTEKKKSLRM
EKEDKVKVADAAEKEANAFAINKDCALEAVDTNLNLKNEELARINFLEKQKUNL
KGCECENGINLSNIDINDEVLHSDDCMSDFDYAEMLRLSOSNLSGKCRKRNQNL
EIKVTPKCSGNERKKTKKRS"

21418..24126

/note="Class 6712"

21783..23439

/gene="OSUNBa0067N01_5"

/note="Putative retroelement"

join(21783..22427, 22632..23195, 23365..23439)

/gene="OSUNBa0067N01_5"

/note="Similar to sp|[P11369] POL2_MOUSE RETROVIRUS-RELATED

POL POLYPROTEIN [CONTAINS"

/codon_start=1

/product="Putative retroelement"

/protein_id="AAK98726_1"

/db_xref="GI: 15451602"

/translation="M0NWEQYKRCQKOEUNGKIEDIDKCKCERAYGHTL

AP004190/c LOCUS AP004190 DNA linear PIN 05-FEB-2004
 DEFINITION *Oryza sativa* (japonica cultivar group) genomic DNA, chromosome 8,
 BAC clone:QJ1506_F01 .
 ACCESSION AB004190
 VERSION 3
 KEYWORDS .
 SOURCE *Oryza sativa* (japonica cultivar group)
Buxaryota; *Viridiplantae*; *Streptophyta*; *Embryophyta*; *Tracheophyta*;
Spermatophyta; *Magnoliophyta*; *Liliopsida*; *Poales*; *Poaceae*;
Erhartoideae; *Oryzeae*; *Oryza*.
 1
 REFERENCE AUTHORS Sasaki,T., Matsuimoto,T. and Yamamoto,K.
 TITLE *Oryza sativa* nippobore (G3) genomic DNA, chromosome 8, BAC
 clone:QJ1506_F01
 JOURNAL Submitted Only in Database (2001)
 2 (bases 1 to 121202)
 REFERENCE AUTHORS Sasaki,T., Matsuimoto,T. and Yamamoto,K.
 TITLE Direct Submission
 JOURNAL Submitted (20-SPR-2001) *Takuji Sasaki*, National Institute of
 Agrobiological Sciences, Rice Genome Research Program; *Kannondai*
 2-1-2, *Tsukasa*, Ibaraki 305-8602, Japan
 (E-mail: tsasaki@nias.affrc.go.jp, URL: <http://rgp.dna.affrc.go.jp/>,
 Tel: 81-298-38-7441, Fax: 81-298-38-7468)
 On Feb 4, 2004 this sequence version replaced gi:37591144.
 Genes were predicted from the integrated results of the following:
 GENSCAN (<http://CCR-001.mit.edu/GENSCAN.html>), FGENESH
 (<http://www.softberry.com/>), GeneMark⁺
 (<http://opala.csail.mit.edu/GenomeMark/>), GlimmerM
 (http://www.tigr.org/tdb/glimmer3/glmr_form.html), RiceHMM
 (<http://bioinformatics.iastate.edu/cgi-bin/s.cgi>), SINA4
 (<http://globin.cse.psu.edu/html/docs/sina4.html>), Gapp2
 (<http://www.tigr.org/software/glimmerm/>) and BLASTX. The
 genomic sequence was searched against NCBI NonRedundant Protein
 database, nr (<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA (s)
 sequence database at RGP or DBJ. Protein homologs of the coding
 regions were searched against NCBI NonRedundant Protein database
 with BLASTP. ESTs represent the identified cDNA sequences using
 BLASTN with the corresponding DBJ accession no. and RGP clone ID.
 Full-length cDNAs represent the identified cDNA sequences using
 BLASTN with the corresponding DBJ accession no.
 A gene with identity or significant homology to a protein is
 classified based on the protein name to indicate the homology level
 such as same name, 'putative-' and '-' like protein'. A gene without
 significant homology to any protein but with full-length cDNA or
 EST homology (covering almost the entire length of partial
 sequence) is classified as an 'unknown' protein. A gene predicted
 by two or more gene prediction programs is classified as a
 'hypothetical' protein according to IRGSP standard. A gene
 predicted by a single gene prediction program is also classified as a
 'probable' 'hypothetical' protein and is included as a
 miscellaneous feature of the sequence.
 The orientation of the sequence is from -21M13 to M13rev of the BAC
 QJ134_H03 (DBJ: AP003892) at 5' end and an overlap with
 QJ134_H03 (DBJ: AP003893) at 3' end. The sequence was generated by
 combining Mononato and RGP-Japan sequencing data. Detailed
 information on overlap and assembly quality together with
 annotation of this entry is available at
<http://rgp.dna.affrc.go.jp/GenomeSeq.html>.

FEATURES source 1. 121202
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="Genomic DNA"
 /cultivar="Nippobore"
 /db_xref="taxon:39947"
 /chromosome="8"
 /clone="QJ1506_F01"
 /gene="QJ1506_F01.1"
 /misc_feature 8688. .9203
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 /misc_feature 8688. .9203

/gene="QJ1506_F01.1"
 /note="hypothetical ORF
 predicted by GENSCAN
 this category is not included in IRGSP standard"
 gene complement (9367 .945)
 /gene="QJ1506_F01.2"
 /note="hypothetical ORF
 predicted by GlimmerM
 this category is not included in IRGSP standard"
 join(10223 .10802 .10833 .11368)
 /gene="QJ1506_F01.3"
 /join(10223 .10802 .10893 .11368)
 /gene="QJ1506_F01.3"
 /note="En/Spm-related transposon protein-like"
 12911 .15439
 /gene="QJ1506_F01.4"
 /join(<12911 .12978 ,15088 .15439)
 /gene="QJ1506_F01.4"
 /note="Start and end point are not identified"
 join(12911 .12978 ,15088 .15439)
 /gene="QJ1506_F01.4"
 /note="predicted by GENSCAN etc."
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 /db_xref="GI:42408125"
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 PPLLIPVSSSVANPTDDEGCRCYCSPSPSPLAQAPPLLPTPVASSSSSGRRG
 PPLLIPVSSSVANPTDDEGCRCYCSPSPSPLAQAPPLLPTPVASSSSSGRRG
 PPLLIPVSSSVANPTDDEGCRCYCSPSPSPLAQAPPLLPTPVASSSSSGRRG
 PPLLIPVSSSVANPTDDEGCRCYCSPSPSPLAQAPPLLPTPVASSSSSGRRG
 complement (15585 .15528)
 /gene="QJ1506_F01.5"
 /note="contains full-length cDNA (s) : AK06964"
 /codon_start=1
 /product="putative arabinogalactan protein"
 /protein_id="BAD09265.1"
 /db_xref="GI:42408126"
 /translation="MMEKSAAMMVTILLCCSISPAFAQKHGPPAAAASLPPSPAP
 SLAARSHTATSDSLSLTAHYHALPRYSSAEFNLLGGAASPVPLAGGYTVNTVD
 MGTVYVGSMMSNPKISSSTYSTRPVAYEDVRLPQMTRDPPMAPSAPAPDKP
 ASDAASPLPKSSSAKAKABDKKSSSSPPSRGAGIAGYFLALLASASAGLILIC"
 complement (15773 .16597)
 /gene="QJ1506_F01.5"
 /note="contains full-length cDNA (s) : AK06964"
 /codon_start=1
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 /protein_id="BAD09265.1"
 /db_xref="GI:42408126"
 /translation="MMEKSAAMMVTILLCCSISPAFAQKHGPPAAAASLPPSPAP
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 MGTVYVGSMMSNPKISSSTYSTRPVAYEDVRLPQMTRDPPMAPSAPAPDKP
 ASDAASPLPKSSSAKAKABDKKSSSSPPSRGAGIAGYFLALLASASAGLILIC"
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 /gene="QJ1506_F01.5"
 /note="predicted by GlimmerM etc."
 /codon_start=1
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 /protein_id="BAD09265.1"
 /db_xref="GI:2408127"
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 predicted by GlimmerM
 this category is not included in IRGSP standard"
 /gene="QJ1506_F01.8"
 /note="hypothetical ORF
 predicted by GlimmerM
 this category is not included in IRGSP standard"
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mRNA	complement(join(<21845..22103,22435..22758,23298..>23434))	RESULT 12	AP003883/c	135914 bp	DNA	linear	PLN 05-FEB-2004
	/gene="OJ1506_F01.8"	LOCUS	AP003883	Oryza sativa (japonica cultivar-group)	genomic DNA	chromosome 8,	
	/note="start and end point are not identified"	DEFINITION		BAC clone:OJ1134_H03.			
CDS	complement(join(21845..22103,22435..22758,23298..>23434))	ACCESSION	AP003883				
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	/note="predicted by GENESH etc."	KEYWORDS					
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	/product="hypothetical protein"	ORGANISM		Oryza sativa (japonica cultivar-group)			
	/protein_id="BAD09268.1"			Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;			
	/db_xref="GI:42408128"			Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
	/translation="IMRLNLCRVAAGEDKHTNFGRRGNENDGLPLRFMLGRKKTRGSRLS			Ehrhartoideae; Oryzae; Oryza.			
	MLRSLSLFSSTSATRDSLSSLRHPLAFAFSSRWRPHLPLRPHYVARNCHKLEVESEBAIRTCIDDF						
	EAQFLNIDIGSKQSTRDESSARCCFSSHELPIDADSQGCDSPHRTYFVLYGESED						
	TYRPFPTSTRFSTVSGRVT"						
gene	24422..24998	AUTHORS	Sasaki, T., Matsumoto, T. and Yamamoto, K.				
	/gene="OJ1506_F01.9"	TITLE	Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC				
mRNA	24422..24998	JOURNAL	clone:OJ1134_H03				
	/gene="OJ1506_F01.9"	REFERENCE	Published Only in Database (2001)				
CDS	24485..24992	AUTHORS	2 (bases 1 to 135914)				
	/gene="OJ1506_F01.9"	TITLE	Direct Submission				
	/note="contains full-length cDNA (S) : AK107730"	AUTHORS	Sasaki, T., Matsumoto, T. and Yamamoto, K.				
	/codon_start=1	JOURNAL	Submitted (09-JUN-2001) Takuji Sasaki, National Institute of				
	/product="calcium-binding EF-hand family protein-like"	REFERENCE	Agrobiological Sciences, Rice Genome Research Program, Kannondai				
	/protein_id="BAD09268.1"	AUTHORS	2-1-2, Tsukuba, Ibaraki 305-8602, Japan				
	/db_xref="GI:42408129"	JOURNAL	(E-mail:tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/				
	/translation="MSVETIDGSTYRSFVDEAANASVTDGGRFALADDGIVLSYAD	COMMENT	Tel:81-298-38-7458)				
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 SOURCE Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 134058)
 AUTHORS Buell,C.R., Yuan,Q., Moffat,K.S., Hill,J.N., Jenkins,C.N.,
 Burr,P.C., Zismann,V., Pai,G., Bowman,C.L., Fujii,C.Y.,
 vanaken,S.E., Bowman,J., Craven,C.L., Utterback,T.R., Khalak,H.,
 Feldblyum,T.V., Quackenbush,J., White,O., Salzberg,S.L. and
 Fraser,C.M.
 TITLE Oryza sativa chromosome 10 BAC OSJNBA0055P24 genomic sequence
 JOURNAL Unpublished
 2 (bases 1 to 134058)
 AUTHORS Buell,R.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-2000) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA
 3 (bases 1 to 134058)
 REFERENCE 3
 AUTHORS Buell,R.
 TITLE Direct Submission
 JOURNAL Submitted (15-SEP-2000) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, rbuell@igr.org
 4 (bases 1 to 134058)
 REFERENCE 4
 AUTHORS Buell,R.
 TITLE Direct Submission
 JOURNAL Submitted (22-SEP-2000) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, rbuell@igr.org
 5 (bases 1 to 134058)
 REFERENCE 5
 AUTHORS Buell,R.
 TITLE Direct Submission
 JOURNAL Submitted (14-OCT-2000) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, rbuell@igr.org
 COMMENT On Sep 15, 2000 this sequence version replaced gi:8272680.
 Address all correspondence to: rice@tigr.org
 BAC clone OSJNBA0055P24 is from Oryza sativa chromosome 10
 The orientation of the sequence is from SP6 to T7 end of the BAC
 clone.
 Genes were identified by a combination of several methods: Gene
 prediction programs including GenScan⁺ (Chris Burge,
<http://CGR-081.mit.edu/GENSCAN.html>), GeneMarkTM (Mark Borodovsky,
<http://genemark.biology.gatech.edu/GeneMark/>), and GeneSplitter
 (Mihaela Pertea and Steven Salzberg, contact mpertea@igr.org).
 Genes without protein or EST similarity, that are predicted by more
 than two gene prediction programs over most of their length are
 annotated as hypothetical proteins. Genes encoding tRNAs are
 predicted by tRNAscan-SE (Sean Eddy,
<http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are
 identified by repeatmasker (Arian Smit,
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>).
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3	1772	100.0	2668	4	AMP24791			Aaf24791 Complete
4	1686	95.1	1686	4	AMP24790			Aaf24790 Nucleotid
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c	7	87.8	5.0	2000	8	ADJ40841		Adj40841 Plant cDN
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c	9	85.8	4.8	5579	6	AAI46938		Aai46938 Rice lesi
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c	20	80.4	4.5	12120	6	AAS96695		Aas96695 Rice DMT1
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 OM nucleic - nucleic search, using SW model
 Run on: November 17, 2004, 09:30:30 ; Search time 824 Seconds
 (without alignments)
 11288.804 Million cell updates/sec

Title: US-10-009-570-1
 Perfect score: 1772
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Scoring table: IDENTITY_NUC
 Gapoff 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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 Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

ALIGNMENTS									
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ID AAF24785 standard; DNA: 1772 BP.									
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XX AAF24785;									
XX DT 20-APP-2001 (first entry)									
XX DE Nucleotide sequence of a rice sucrose synthase 3 (RSuS3) promoter.									
XX KW Rice; sucrose synthase 3 promoter; RSuS3 promoter; endosperm expression; transgenic plant; carbohydrate metabolism; sucrose metabolism; ss.									
XX OS Oryza sativa.									
XX FN WO200078975-A2.									
XX PD 28-DEC-2000.									
XX PF 15-JUN-2000; 2000WO-GB002641.									
XX PR 17-JUN-1999; 99GB-00014210.									
XX (DANI) DANISCO AS.									
XX PI Donaldson IA, Rasmussen TB;									
XX DR WPI; 2001-071398/08.									
XX PR 17-JUN-1999; 99GB-00014210.									
XX (DANI) DANISCO AS.									
XX PF Rice sucrose synthase 3 promoter obtainable from plant genus <i>Oryza</i> , useful for expressing nucleotide sequence of interest in specific tissue or cell type e.g. endosperm.									
XX PR Claim 1; Page 142; 144pp; English.									
XX CC The present sequence represents a rice sucrose synthase 3 (RSuS3) promoter. The RSuS3 promoter has low homology with the RSuS1 and RSuS2 promoters (7.7% and 4.8%, respectively). In addition, apart from conserved TATA box and intron splice sites, they have no motifs in common. The promoter can be used to produce a product of interest, especially in the endosperm of a transgenic plant. Preferably, the promoter is used to cause expression of a nucleotide of interest that can affect carbohydrate metabolism, such as sucrose metabolism, in a plant tissue									

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	1772	100.0	1772	4	AMP24785			Aaf24785 Nucleotid
2	1772	100.0	1803	4	AMP24787			Aaf24787 Nucleotid
3	1772	100.0	2668	4	AMP24791			Aaf24791 Complete
4	1686	95.1	1686	4	AMP24790			Aaf24790 Nucleotid
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c	6	97.4	5.5	2000	8	ADA73143		Ada73143 Rice gene
c	7	87.8	5.0	2000	12	ADJ40841		Adj40841 Plant cDN
c	8	86	4.9	86	4	AMP24788		Aaf24788 Nucleotid
c	9	85.8	4.8	5579	6	AAL46938		Aal46938 Rice lesi
c	10	85.4	4.8	2000	8	ADA72816		Ada72816 Rice gene
c	11	84.2	4.8	2000	8	ADJ41087		Adj41087 Plant cDN
c	12	83.2	4.7	900	12	ADG22907		Adg22907 Rice vari
c	13	83	4.7	2000	10	ADC0814		Adc0814 Rice DNA
c	14	81.8	4.6	2000	8	ADA73166		Ada73166 Rice gene
c	15	81.6	4.6	2000	8	ADA71497		Ada71497 Rice gene
c	16	81.6	4.6	2000	8	ADA73455		Ada73455 Rice gene
c	17	81.6	4.6	2000	8	ADA71498		Ada71498 Rice gene
c	18	81	4.6	2000	8	ADA72521		Ada72521 Rice gene
c	19	80.4	4.5	2000	8	ADA72089		Ada72089 Rice gene
c	20	80.4	4.5	12120	6	AAS96695		Aas96695 Rice DMT1
c	21	80.4	4.5	12120	11	ADM35550		Adm35550 DMT polyn

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Db	1741	TAGAGTTCTCCTCCATGGCAAG	1772
RESULT 3			
TD	AAF24791	standard; DNA; 2668 BP.	
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	20-APR-2001	(first entry)	
		Complete nucleotide sequence of a sucrose synthase 3 (RSus3) promoter.	
		Rice; sucrose synthase 3 promoter; RSus3 promoter; endosperm expression; transgenic plant; carbohydrate metabolism; sucrose metabolism; ss.	
		Oryza sativa.	
		W0200078975-A2.	
		28-DEC-2000.	
		15-JUN-2000; 2000WO-GB002641.	
		17-JUN-1999; 99GB-00014210.	
		(DANI-) DANISCO AS.	
		Donaldson IA, Rasmussen TB;	
		WPI; 2001-071398/08.	
		Rice sucrose synthase 3 promoter obtainable from plant genus Oryza, useful for expressing nucleotide sequence of interest in specific tissue or cell type e.g. endosperm.	
		Disclosure: Fig 3; 144pp; English.	
		The present sequence represents a rice sucrose synthase 3 (RSus3) promoter. The RSus3 promoter has low homology with the RSus1 and RSus2 promoters (7.7% and 4.6%, respectively). In addition, apart from conserved TATA box and intron splice sites, they have no motifs in common. The promoter can be used to prepare a product of interest, especially in the endosperm of a transgenic plant. Preferably the promoter is used to cause expression of a nucleotide of interest that can affect carbohydrate metabolism, such as sucrose metabolism, in a plant tissue	
PS	Sequence 2668 BP;	747 A; 519 C; 572 G; 830 T; 0 U; 0 Other;	
CC	Query Match	100.0%	Score 1772;
CC	Best Local Similarity	100.0%	DB 4; Length 2668;
CC	Matches 1772;	Conservative	Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
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CC	DDB	1 ACTTGTAGATATAAAGTAAACTCACAGAAATAATAATTATTCCTTAAATTATAA	60
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CC	DDB	61 AGACGAGTGGTCAAAAGTACAGTAAACTCAAACAAACACACACCCG	180
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CC	QY	181 CACCRNGCAGGCGATGCGATCTAGGTCGGCACATTCAGGTTAACAGCA	240
CC	DDB	181 GATATCTGGTTCTGGTTAACAGGTTCAACATCCCTTAACCTGACAAATAATTGTC	132
CC	QY	1261 GATATCTGGTTCTGGTTAACAGGTTCAACATCCCTTAACCTGACAAATAATTGTC	132

QY	1321	AATTAAATTAACTTTAAGTTTTAACTTAGCCGGAAACCTTGAAGTTGCTGTCG	1380	CC common. The promoter can be used to prepare a product of interest, especially in the endosperm of a transgenic plant. Preferably, the promoter is used to cause expression of a nucleotide of interest that can affect carbohydrate metabolism, such as sucrose metabolism, in a plant tissue
Db	1321	AATTAAATTAACTTTAAGTTTTAACTTAGCCGGAAACCTTGAAGTTGCTGTCG	1380	CC
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QY	781	TAAGATTTACTAACGACATCGCTCATCACACCCAAAGCTAACGCTAC	840	QY
Db	781	TAAGATTTACTAACGACATCGCTCATCACACCCAAAGCTAACGCTAC	840	Db
QY	841	GACCAAGAGTTAGGACTGTGCAATATGGTGCACATATGGTGCACATATGGTGC	900	QY
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QY	901	ATGCCGAATTAGGTGTTCTCATGACGTTCCAACGGCACAGGGTGAAGCAT	960	QY

The present sequence represents a rice sucrose synthase 3 (RSus3) promoter fragment. The RSus3 promoter has low homology with the RSus1 and RSus2 promoters (7.7% and 4.6%, respectively). In addition, apart from conserved TATA box and intron splice sites, they have no motifs in

Db	901	ATCGGAATTCTAGGGTTGTTGTCATGACGCCAACGGCAAGGGTGAAGCT 960	PD 03-JAN-2003.
Qy	961	GCATGCATGGCTTGTGAAACTAAAGTGTACTGGTAATGACATGCTGTTAGCT 1020	XX XX 22-JUN-2001; 2001WO-IB001105.
Db	961	GCATGCATGGCTTGTGAAACAAAGTGTACTGGTAATGACATGCTGTTAGCT 1020	XX PR 22-JUN-2001; 2001WO-IB001105.
			XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Qy	1021	AGTGGCGATGTAAGGCCATGATGCAATGCTATGCAACAAGTATAGTACCGCA 1080	XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
Db	1021	AGTGGCGATGTAAGGCCATGATGCAATGCTATGCAACAAGTATAGTACCGCA 1080	XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
			XX DE 2003-175290/17.
Qy	1081	TGATGGAGCCAGTAACTAATCTATCGAGGGCAAGCTGCAATGGTGTATGGTAT 1140	XX DR
Db	1081	TGATGGAGCCAGTAACTAATCTATCGAGGGCAAGCTGCAATGGTGTATGGTAT 1140	XX PT Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.
Qy	1141	GCACITCTCTCCAGTAATCTAGTGGTAATTCACCCAAAGCTGTCATATGGACAT 1200	XX PT
Db	1141	GCACITCTCTCCAGTAATCTAGTGGTAATTCACCCAAAGCTGTCATATGGACAT 1200	XX PT
Qy	1201	AATTAGTAATTACCAAGGTTACAATCCGGTACCTGCCAAATACTACTCACGATG 1260	XX PS Claim 27; SEQ ID NO 6505; 899p; English.
Db	1201	AATTAGTAATTACCAAGGTTACAATCCGGTACCTGCCAAATACTACTCACGATG 1260	XX CC The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1
Qy	1261	GTATCTCTGGTTTGGTAACCTGGTAAACCGAAATAAGCAAAATTTGTCAA 1320	CC CC comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to the expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
Db	1261	GTATCTCTGGTTTGGTAACCTGGTAAACCGAAATAAGCAAAATTTGTCAA 1320	CC CC
Qy	1321	AATTTTAAATTAAATTAGTTTTAACTTACCTAGCGGGAAACCTGAAAGTTGGTGG 1380	CC CC
Db	1321	AATTTTAAATTAAATTAGTTTTAACTTACCTAGCGGGAAACCTGAAAGTTGGTGG 1380	CC CC
Qy	1381	AGCTGTCCTGGAAAGGAGGGTTTGGTTGGGATTTGTAACCTGGTTACTGCACITCAT 1440	XX SQ Sequence 2000 BP; 520 A; 394 C; 427 G; 658 T; 0 U; 1 Other;
Db	1381	AGCTGTCCTGGAAAGGAGGGTTTGGTTGGGATTTGTAACCTGGTTACTGCACITCAT 1440	Query Match 61.1%; Score 1082.4; DB 8; Length 2000;
Qy	1441	TTTGAACAGATAATTAGTGCACAGAAATCCGGTACCGCA 1500	Best Local Similarity 99.3%; Pred. No. 3.2e-79; Mismatches 6; Indels 2; Caps 1;
Db	1441	TTTGAACAGATAATTAGTGCACAGAAATCCGGTACCGCA 1500	Matches 1098; Conservative 0; Mismatches 6; Indels 2; Caps 1;
Qy	1501	GCTGAAGCTTTACGATCCCCATACGGCCGTTGTCGCAAACTGCCAACGGCA 1560	Qy 669 CGCTTAACTGAGATAAAATTATTCATAGATCATTAACTCATTTTGTGCT 728
Db	1501	GCTGAAGCTTTACGATCCCCATACGGCCGTTGTCGCAAACTGCCAACGGCA 1560	Db 1 CGCTTAACTGAGATAAAATTATTCATAGATCATTAACTCATTTTGTGCT 60
Qy	1561	GAACAGGGTGCATTGTTGGTGTGAAAGCCAGTAAGTAAACAGAAATGCAATGATG 1620	Qy 729 TCGTTCAATTTCCTACCACTTATCAACCATACTGTCAACTGTCACCTTGTGCT 728
Db	1561	GAACAGGGTGCATTGTTGGTGTGAAAGCCAGTAAGTAAACAGAAATGCAATGATG 1620	Db 61 TCGTTCAATTTCCTACCACTTATCAACCATACTGTCAACTGTCACCTTGTGCT 60
Qy	1621	GAGGACAGGGAACTGGGACACATGCCAGCCAGGCTCCCTGACATGGCCACCTGGTCA 1680	Qy 789 ACTAAAGACATGCGCTCATCACACCAAGGCTCAGCTGGTGCCTCTGACACAGA 848
Db	1621	GAGGACAGGGAACTGGGACACATGCCAGCCAGGCTCCCTGACATGGCCACCTGGTCA 1680	Db 121 ACTAAAGACATGCGCTCATCACACCAAACTCCCTCACGCTGGTGCCTCTGACACAGA 180
Qy	1681	TAATAA 1686	Qy 849 GTTTAGGCACCTTGCAACATATGGCTGGATGAACTACTGATGGCTGGCAATGGTCA 908
Db	1681	TAATAA 1686	Db 181 GTTTAGGCACCTTGCAACATATGGCTGGATGAACTACTGATGGCTGGCAATGGTCA 240
			Qy 909 TTTAGGCCTCGTTCATGCGCTTCCAAACGGCAACGGCTCAACGGCATGGCTGGCAATGGTCA 968
			Db 241 TTTAGGCCTCGTTCATGCGCTTCCAAACGGCAACGGCTCAACGGCATGGCTGGCAATGGTCA 300
Qy	969	GGCTCTGTGAAACAAAAAGTTACTGTTAAATGACATGCTGCTGAGTGTAGTTAGCA 1028	Qy 969 GGCTCTGTGAAACAAAAAGTTACTGTTAAATGACATGCTGCTGAGTGTAGTTAGCA 1028
Db	301	GGCTCTGTGAAACAAAAAGTTACTGTTAAATGACATGCTGCTGAGTGTAGTTAGCA 360	Db 301 GGCTCTGTGAAACAAAAAGTTACTGTTAAATGACATGCTGCTGAGTGTAGTTAGCA 360
Qy	1029	GAATGCAAGGCCATGATGAACTGATGAACTGATGAACTGATGAACTGATGATGGT 1088	Qy 1029 GAATGCAAGGCCATGATGAACTGATGAACTGATGAACTGATGATGGT 1088
Db	361	GAATGCAAGGCCATGATGAACTGATGAACTGATGATGGT 420	Db 361 GAATGCAAGGCCATGATGAACTGATGATGGT 420
Qy	1089	AGCCAGCTAACTATCTATCGGAGGGCAAGCTGTCGATGTTGATGCACTCT 1148	Qy 1089 AGCCAGCTAACTATCTATCGGAGGGCAAGCTGTCGATGTTGATGCACTCT 1148
Db	421	AGCCAGCTAACTATCTATCGGAGGGCAAGCTGTCGATGTTGATGCACTCT 480	Db 421 AGCCAGCTAACTATCTATCGGAGGGCAAGCTGTCGATGTTGATGCACTCT 480
Qy	1149	CTCCAGTAATTCTAGGTGAATTTCACCCAAAGCTGTCGATGTTGATGCACTCT 1208	Qy 1149 CTCCAGTAATTCTAGGTGAATTTCACCCAAAGCTGTCGATGTTGATGCACTCT 1208
Db	481	CTCCAGTAATTCTAGGTGAATTTCACCCAAAGCTGTCGATGTTGATGCACTCT 540	Db 481 CTCCAGTAATTCTAGGTGAATTTCACCCAAAGCTGTCGATGTTGATGCACTCT 540
			XX WO2003000898-A1.
			XX

XX The invention relates to plant nucleotide sequences that direct seed-, leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced ecological dominance or dwarfism, early flowering or altered metabolic pathways. This sequence represents a plant nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPRO at seqdata.uspto.gov/sequence.html.

```

Query Match      4.8%; Score 84.2; DB 12; Length 2000;
Best Local Similarity 88.0%; Pred. No. 1e-11;
Matches 103; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
Query 3 TTTAGGATAATAAAGTAAGTCACAGGAAATAATAATTCCAAATTTTTATAAG 62
Db 3.44 TTGGGATAATAAAGTAAGTCACAAAATTTAAATAATTTC AATTTTTTATAG 286
Query 63 ACGAGTGGTCAACAGTCAAGTCAAAGTCAAACCTCAAATTTCCCTTATATGGACTAT 119
Db 285 ATGAGTGGTCAACAGTCAAGGCAAGGAAACTCAAATCCCTTATATGGACGGAT 229

```

XX ADG27907;
 XX AC
 XX DT 11-MAR-2004 (first entry)
 XX Rice variation-containing genome region DNA SeqID22.
 XX rice variety; rice genome; quality control; adulterant detection
 XX small trader protection; consumers protection; ds.
 KW

OS *Oryza sativa*.
XX

```

variation FT replace(175,A)
variation FT /*tag= a
variation FT /standard name= "Single nucleotide polymorphism"
variation FT replace(197,A)
variation FT /*tag= b
variation FT /standard name= "Single nucleotide polymorphism"
variation FT replace(231,A)
variation FT /*tag= c
variation FT /standard name= "Single nucleotide polymorphism"
variation FT replace(271,T)
variation FT /standard name= "Single nucleotide polymorphism"

```

```

FT variation      /* tag= d      "Single nucleotide polymorphism"
FT variation      replace(285,T)
FT variation      /* tag= e      "Single nucleotide polymorphism"
FT variation      replace(346,A)
FT variation      /* tag= f      "Single nucleotide polymorphism"
FT variation      replace(381,T)
FT variation      /* tag= g      "Single nucleotide polymorphism"
FT variation      replace(384,T)

```

RESULT 13
 ADC08414/C
 ID ADC08414 standard; DNA; 2000 BP.
 XX
 AC ADC08414;
 XX
 DT 18-DBC-2003 (first entry)
 XX
 DE Rice DNA sequence Seq ID719 related to grain filling.
 XX
 KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; Peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX
 OS Oryza sativa.
 XX
 PN WO2003000905-A2.
 XX
 PD 03-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-IB002450.
 XX
 PR 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 20-DEC-2001; 2001US-0342327P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 DR WPI; 2003-229341/22.
 XX
 PT New Plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 XX
 Disclosure: SEQ ID NO 719; 130pp; English.
 XX
 This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is a
 CC DNA sequence of a rice gene promoter. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC [ftp://wipo.int/pub/publishedpc_sequences](http://wipo.int/pub/publishedpc_sequences).
 XX
 Sequence 2000 BP; 480 A; 520 C; 441 G; 559 T; 0 U; 0 Other;
 SQ Query Match 1 ACTTTAGATAATAAGTACAGAAATAATAATTCAAAATTCTTATAATATGGGAC 115
 Best Local Similarity 4.7%; Score 83; DB 10; Length 2000;
 Matches 95; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ACTTTAGATAATAAGTACAGAAATAATAATTCAAAATTCTTATAATATGGGAC 60
 DB 1145 ACTTTAGATAATAAGTACAGAAATAATAATTCAAAATTCTTATAATATGGGAC 1086
 QY 61 AGACCAAGTGTCAAACAGTACAGTAAACTCAAATTCCTTATATTATGGGAC 115
 DB 1002 AAACGAGTGTCAAACAGTACAGTAAACTCAAATTCCTTATAATAGAGAC 948
 RESULT 15
 ADA71497
 ID ADA71497 standard; DNA; 2000 BP.
 XX
 AC ADA71497;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Rice gene, SEQ ID 6492.

XX Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.

XX *Oryza sativa*.

XX WO200300898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y, Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX DR 2003-175290/17.

PT Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

XX PS Claim 27; SEQ ID NO 4820; 899pp; English.

CC The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection, M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

XX Sequence 2000 BP; 713 A; 326 C; 345 G; 616 T; 0 U; 0 Other;

Query Match 4.6%; Score 81.6; DB 8; Length 2000;
 Best Local Similarity 87.1%; Pred. No. 5.1e-11;

Matches 101; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

Qy 1 ACTTTAGATAAACTAAGTCAAGAAATAAAATAATATTCC-AATTTTTAT 59
 Db 423 ACTGTGGATATAAGTAAAGTCAAAATGAAATAATAATTTCAAAATTGAT 482

Qy 60 AAGACGGAGTGGTCAAAAGTAAAGTAAACTCAAATTCCTTATATGGAC 115
 Db 483 AAGACGGAGTGGTCAAAATAAAGCAAAATCCTTATATGAGAC 538

Search completed: November 17, 2004, 11:07:15
 Job time : 830 secs

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OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 10:46:50 ; Search time 174 Seconds
 Perfect score: 1772

Title: US-10-009-570-1

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 824507 seqs, 355194441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA:
 1: /cgn2_6_ptodata/1/ina/5A_COMB.seq:
 2: /cgn2_6_ptodata/1/ina/5B_COMB.seq:
 3: /cgn2_6_ptodata/1/ina/6A_COMB.seq:
 4: /cgn2_6_ptodata/1/ina/6B_COMB.seq:
 5: /cgn2_6_ptodata/1/ina/PCNTS_COMB.seq:
 6: /cgn2_6_ptodata/1/ina/backfilesi.seq:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	47.2	2.7	7218	1	US-08-232-463-14
C 2	45.6	2.6	640681	4	Sequence 14, Appli
C 3	43	2.4	832	4	Sequence 1, Appli
C 4	42.8	2.4	1141	4	Sequence 2813, Appli
C 5	42	2.4	3602	4	Sequence 22, Appli
C 6	40.2	2.3	640681	4	Sequence 1, Appli
C 7	39	2.2	3738	4	Sequence 1, Appli
C 8	39	2.2	3926	4	Sequence 3978, AP
C 9	38.8	2.2	8607	4	Sequence 4015, AP
C 10	38.6	2.2	450	4	Sequence 71, Appli
C 11	38.4	2.2	81001	4	Sequence 1239, Appli
C 12	38.2	2.2	640681	4	Sequence 1, Appli
C 13	38.2	2.2	195	4	Sequence 8025, Appli
C 14	37.8	2.2	1141	4	Sequence 2330, AP
C 15	37.6	2.1	1242	4	Sequence 22, Appli
C 16	37.8	2.1	3758	3	Sequence 352, Appli
C 17	37.8	2.1	4383	3	Sequence 1, Appli
C 18	37.8	2.1	4383	6	Sequence 2, Appli
C 19	37.8	2.1	4383	6	Patent No. 5175095
C 20	37.8	2.1	6070	4	Patent No. 5177307
C 21	37.6	2.1	1017	4	Sequence 10, Appli
C 22	37.6	2.1	1092	3	Sequence 1003, Appli
C 23	37.6	2.1	2031	3	Sequence 1876, Appli
C 24	37.6	2.1	2031	3	Sequence 5, Appli
C 25	37.6	2.1	3285	4	Sequence 4, Appli
C 26	37.6	2.1	11131	4	Sequence 28, Appli
C 27	37.4	2.1	3126	4	Sequence 3912, Appli

ALIGNMENTS

RESULT 1	US-08-232-463-14/C	Sequence 14, Application US/08232463
;	;	Patent No. 5670367
;	;	GENERAL INFORMATION:
;	;	APPLICANT: DORNER, F.
;	;	APPLICANT: SCHIEFLINGER, F.
;	;	APPLICANT: FALKNER, F. G.
;	;	TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;	;	NUMBER OF SEQUENCES: 52
;	;	CORRESPONDENCE ADDRESS:
;	;	ADDRESSEE: Foley & Lardner
;	;	STREET: 1800 Diagonal Road, Suite 500
;	;	CITY: Alexandria
;	;	STATE: VA
;	;	COUNTRY: USA
;	;	ZIP: 22313-0399
;	;	COMPUTER READABLE FORM:
;	;	MEDIUM TYPE: Floppy disk
;	;	COMPUTER: IBM PC compatible
;	;	OPERATING SYSTEM: PC-DOS/MS-DOS
;	;	SOFTWARE: Patent in Release #1.0, Version #1.25
;	;	APPLICATION DATA:
;	;	APPLICATION NUMBER: US/08/232,463
;	;	FILING DATE:
;	;	CLASSIFICATION: 435
;	;	PRIOR APPLICATION DATA:
;	;	APPLICATION NUMBER: US/07/935,313
;	;	FILING DATE:
;	;	APPLICATION NUMBER: EP 91 114 300.6
;	;	FILING DATE: 26-AUG-1991
;	;	ATTORNEY/AGENT INFORMATION:
;	;	NAME: BENT, Stephen A.
;	;	REGISTRATION NUMBER: 29,768
;	;	REFERENCE/DOCKET NUMBER: 30472/114 IMMU
;	;	TELECOMMUNICATION INFORMATION:
;	;	TELEPHONE: (703) 836-9300
;	;	TELEFAX: (703) 683-4109
;	;	TELEX: 899149
;	;	INFORMATION FOR SEQ ID NO: 14:
;	;	SEQUENCE CHARACTERISTICS:
;	;	LENGTH: 7218 base pairs
;	;	TYPE: nucleic acid
;	;	STRANDEDNESS: single
;	;	TOPOLOGY: linear
;	;	IMMEDIATE SOURCE:
;	;	CLONE: pt2cpt-FLs
;	;	US-08-232-463-14
;	;	Query Match

FEATURE: NAME/KEY: promoter
LOCATION: (1). (1141)
OTHER INFORMATION: consensus sequence of A.t., I.a., and B.n. FAEL promoters
IS-09-806-708B-22

Query Match	Score 2.4%	DB 4	Length 1141;
Best Local Similarity	9.9%	Pred. No. 0 038;	
Matches	56	Mismatches	238;
Indels	3	Gaps	2;
Y	212 ATTGAGGGTCGGCAGTAGACGAGTTACCTACACAATGCTGCTTCAGTGAGCTAGCTGTG 271		
b	149 WTTMCMDKDDKRTRWWKRNNAATGDDDTKYHMMNNNGCBTVWTRYKTDIDRWKRR 208		
Y	272 CATGTTCTGTCCTGCATTACATTGGAGGAGAGCTAGCAAAGTTGAGAAACAACT 331		
b	209 MNYGMBWKRWNNSYDVTYWWNDDMCCKVREKWRTRGRMRNNMVAANBTAAHRRYNNNGWT 268		
Y	332 GATAATCCATTGTCAGGGAGAACATGGAGAAACAGGGGCTGGAGACAGGGAG 391		
b	269 BAMYARRWTMNNNNNPKAMCKRAKYWGWNRAEVNSTTWSKTTVRTSCVANNCRAG 328		
Y	392 CAGGTGACCGTAGTTCTGAGGGCTGAACCCATCTGCGAAATCCCGAGATGGTTGTG 451		
b	329 DANKDHWK - -WWSAAGGVWNNNNNNWTKYKARHARWDWVWHSWKKWHAAYHSR 386		
Y	452 TCAATTCACAACTTGCAAGTCCTTCAGATTGGTNGCATGTTCAACCGTAGTACTCTGAAA 511		
b	387 KRWTKRKTWVNNNNNGTTMNMKRMWAWYWKMDMDWBCTYNNNNNGGRTYYGWTNKWKWT 446		
Y	512 ATGA-AGTGTAAATACCTTGAAGAACCTTCATGGAGCATGCCCTCAGGGGATTGCT 570		
b	447 YYKKWANCKWRAWDEKTCIHNNTTWWMKTYWNNNCWPKSMTNKGSKHRBAAVYTWWWW 506		
Y	571 AGAAAAAATAAAATAATGACTTTGGAGTTAGATTTAGGGTTG 630		
b	507 WRYYHANNNNWDYWWKACTWYKYBUCSKWNNNNYAWTKSWSWNTSRYRKTNNSWRW 566		
Y	631 TTCCATCGTAGCTACTATTCTACTATTGCAAGTTAACCGCTAATAGCTAGATAAAAT 690		
b	567 RSDTRSMGRANNYARABHYGKWNTRWWBWSHTWBHRAGAHYHMMYBAKCHCMKAW 626		
Y	691 TTATCTATGATCATTTATAATCTTGTGTTCTGTTCAATTCTPACCACTTA 750		
b	627 YKAKKYGAGGSSNNNNNNNNNNNNNNNNNATCARDYYAASRKYWAMANAKWYKBAANNA 686		
Y	751 TCAACCATAGTCAACTGATCAACTGATCAAT 774		
b	687 YYTHANNNNGCWNNAATDTRRTMWK 710		

RESULT 5
IS-09-402-929-1
Sequence 1, Application US/09402929
Patent No. 6410825

GENERAL INFORMATION:
APPLICANT: Temple University - Of the Commonwealth System of Higher Education
APPLICANT: Toscani, Antonio
APPLICANT: Hatton, Kimi
APPLICANT: Reddy, E. P.
TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEIDEL, GONDA, LAVORGNA & MONACO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,929
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US98/06896
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Monaco, Daniel A.
 REGISTRATION NUMBER: 30,480
 REFERENCE/DOCKET NUMBER: 6056-214 PC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-8383
 TELEFAX: (215) 568-5549
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3602 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US -09-402-929-1.

Query Match 2.4%; Score 42; DB 4; Length 3602
 Best Local Similarity 52.9%; Pred. NO. 0.12; Mismatches 80;
 Matches 90; Conservative 0; Mismatches 80;

Qy	3	TTTAAATAAAGTAAGTCACAGGAAATAATAATAATAATAT
Db	3433	TGTTGGTTTAAGTAGTTCTAAATGTCATAATAAATATAAT
Qy	63	ACGAGTGGTAAACGTAACGTAACGTAACGTAACGTAACGTA
Db	3493	TTATATTGGGGTCATAATAATAATCTGGTGTATGTTAT
Qy	123	ATGGGACGGGGAACTAGAAGATTGTAGCCAGAAAAAAC
Db	3553	TTTGTGTTAAAAAAAGAAAAAAAGAAAAAAAGAAAAAA

RESULT 6
 US -09-790-988-1
 Sequence 1, Application US/09790988
 Parent No. 6632935
 GENERAL INFORMATION:
 APPLICANT: SHIGENOBU, SHUJI
 APPLICANT: WATANABE, HIDEMI
 APPLICANT: HATTORI, MASAHIRA
 APPLICANT: SATAKI, YOSHIOUKI
 TITLE OF INVENTION: GENOME DNA OF BACTERIAL Symbiont
 FILE REFERENCE: 081356/0159
 CURRENT APPLICATION NUMBER: US/09/790,988
 CURRENT FILING DATE: 2001-02-23
 PRIOR APPLICATION NUMBER: JP2000-107160
 PRIOR FILING DATE: 2000-04-07
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 640681
 TYPE: DNA
 ORGANISM: Buchnera sp.
 US -09-790-988-1.

Query Match 2.3%; Score 40.2; DB 4; Length 640681
 Best Local Similarity 53.5%; Pred. NO. 6.7; Mismatches 73; Matches 84; Conservative 0; Mismatches 73;

Qy	640	AGCTTATTTCTCTATGCAAGTTAACCGGTTAAAGTCAG
Db	125520	AAATAAAATTATTTTTAAAGTTTAATGCTTAAATACTAC
Qy	700	AGATCATTAAATCATTTTAAAGTTGCTCCCTTCAATTTC

RESULT 8
 US-09-710-279-4015
 i Sequence 4015 Application US/09710279
 i Pat. No. 670492
 i GENERAL INFORMATION:
 i APPLICANT: KIMMERLY, WILLIAM JOHN
 i TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 i FILE REFERENCE: PU34800US
 i CURRENT APPLICATION NUMBER: US/09/710,279
 i CURRENT FILING DATE: 2000-11-09
 i PRIOR APPLICATION NUMBER: 60/164,258
 i PRIOR FILING DATE: 1999-11-09
 i NUMBER OF SEQ ID NOS: 4472
 i SOFTWARE: PatentIn Ver. 2.1
 i SEQ ID NO: 3978
 i LENGTH: 3738
 i TYPE: DNA
 i ORGANISM: Artificial Sequence
 i FEATURE: Description of Artificial Sequence: synthetic
 i OTHER INFORMATION: nucleic acid sequence
 US-09-710-279-3978

Query Match 2.2%; Score 39; DB 4; Length 3738;
 Best Local Similarity 52.1%; Pred. No. 0.9;
 Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 559 AGGGATTAGCTAAGAAAAAAATAAAGTACTTTCGAAACTTAATTTGGAGTTAG 618
 Db 111 AAGTGTATCAATGTAAATCAATCTGTTTATGTTAATGTTGCTTAACA 170
 Qy 619 ATTTAGGTGTTCCATGTAGTTCTACTATGGAGTTAACCGCTTAATAGT 678
 Db 171 ATCATGTACTAAATCTGCTGTTACTCTTTCATGATGTCACCTCCTATAGT 230
 Qy 679 CAGATAAAATTATPATCATPATATAATCATTTTGTAGT 725
 Db 231 AACTATTATTAAATTAAATTAAATTCTTTTATTAATT 277

RESULT 9
 US-10-204-708-71
 i Sequence 71 Application US/10204708
 i Patent No. 667771
 i GENERAL INFORMATION:
 i APPLICANT: OLEK, Alexander
 i APPLICANT: PIERENBROCK, Christian
 i APPLICANT: BERLIN, Kurt
 i TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
 i TITLE OF INVENTION: by Assessing DNA Methylation
 i FILE REFERENCE: 5013-1012
 i CURRENT APPLICATION NUMBER: US/10/204,708
 i CURRENT FILING DATE: 2003-05-06
 i PRIOR APPLICATION NUMBER: PCT/EP01/03971
 i PRIOR FILING DATE: 2001-04-06
 i PRIOR APPLICATION NUMBER: DE 10019058.8
 i PRIOR FILING DATE: 2000-04-06
 i PRIOR APPLICATION NUMBER: DE 10019173.8
 i PRIOR FILING DATE: 2000-04-07
 i PRIOR APPLICATION NUMBER: DE 10032519.7
 i PRIOR FILING DATE: 2000-06-30
 i PRIOR APPLICATION NUMBER: DE 10043826.1
 i PRIOR FILING DATE: 2000-09-01
 i NUMBER OF SEQ ID NOS: 98
 i SEQ ID NO: 71
 i LENGTH: 8607
 i TYPE: DNA
 i ORGANISM: Artificial Sequence
 i FEATURE:
 i OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-204-708-71

Query Match 2.2%; Score 38.8; DB 4; Length 8607;
 Best Local Similarity 51.8%; Pred. No. 1.6;
 Matches 88; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 574 AAAAAGAAAAATAAATTAATCTACTTTCGAAACTTAATTTGGAGTTAACCGCTTAATAGT 633
 Db 7620 AAAAGATATTACGTGTGATGATTATAATTATATTGAATTGTAGTTGTTAT 7679
 Qy 634 CATCGTAGTGTATTCTACTATGGAGTTAACCGCTTAATAGTCAATAAATT 693
 Db 7680 TAATTTAGGTGTTTGTAGTTAGTTAGTGTGCTGTTAGTTAAATTGAAAGTTCTA 7739
 Qy 694 ATCTATAGTATTATAATCATTTAGTGTGCTGTTAGTTAAATTGAAAGTTCTA 743
 Db 7740 TTATATGTTATTTAGGTATGTTTGTAGTTAAATTGTTA 7789

RESULT 10
 US-09-270-767-12394
 i Sequence 12394 Application US/09270767
 i Patent No. 6703491
 i GENERAL INFORMATION:
 i APPLICANT: Homburger et al.
 i TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 i FILE REFERENCE: File Reference: 7326-094
 i CURRENT APPLICATION NUMBER: US/09/270,767

Query Match 2.2%; Score 39; DB 4; Length 3926;
 Best Local Similarity 52.1%; Pred. No. 0.92;

RESULT 11
 US-09-270-767-12394
 i Sequence 12394 Application US/09270767
 i Patent No. 6703491
 i GENERAL INFORMATION:
 i APPLICANT: Homburger et al.
 i TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 i FILE REFERENCE: File Reference: 7326-094
 i CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62571
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 12394
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-12394

Query Match 2.2% ; Score 38.6 ; DB 4 ; Length 450 ;
Best Local Similarity 51.4% ; Pred. No. 0.37 ;
Matches 89 ; Conservative 0 ; Mismatches 84 ;
Indels 0 ; Gaps 0 ;

Qy	6 AGATATAAAGTTAAGTCAAGAAAATAATAATTCCAAATTTTATAAGACG 65	OTHER INFORMATION: 20-828-311 : polymorphic base C or T
Db	1 AGACATGTCAGAAACCGAAATAATTATAATAACATAATATATAAA 60	NAME/KEY: exon OTHER INFORMATION: exon 4
Qy	66 AGTGTCAACAGTACAGTAACACTAAACATCCTATAATTGGACTATATTG 125	NAME/KEY: misc feature LOCATION: 15963..17969
Db	61 TAATGTAATACTAAACAAACAAATTCTCTTATTAAATTATAATTAAATA 120	OTHER INFORMATION: 3-regulatory region
Qy	126 GACCGAGGAGGTAGAAGATGTACCCAGAAAACAAACACACC 178	NAME/KEY: allele LOCATION: 1239
Db	121 ATATATATAATAATAATAATAATAATAATAATAATAATAATAATAACC 173	OTHER INFORMATION: 20-828-311 : polymorphic base C or T

RESULT 11
US-09-150-580-1/c
Sequence 1, Application US/09750580
Patent No. 6455980

GENERAL INFORMATION:
APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bihain, Bernard
APPLICANT: Dumas, Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bouquellet, Lydie
APPLICANT: Ebots Reider, Dana
APPLICANT: Salter-Cid, Luisa

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89 US 2,111,111
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,636
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent-ppm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: misc feature
NAME/KEY: exon
LOCATION: 12947..129458
OTHER INFORMATION: exon 1

NAME/KEY: exon
LOCATION: 10946..129456
OTHER INFORMATION: exon 4

NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2

NAME/KEY: exon
LOCATION: 1222..12346
OTHER INFORMATION: 17-42-319.mis

NAME/KEY: primer bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement

NAME/KEY: primer bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-842..1240
NAME/KEY: primer bind
LOCATION: 1238..1246
OTHER INFORMATION: 17-42-319.mis

NAME/KEY: primer bind
LOCATION: 1216..12185
OTHER INFORMATION: 20-853..12185
NAME/KEY: primer bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42..12050
NAME/KEY: primer bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42..12603
NAME/KEY: primer bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828..1377
NAME/KEY: primer bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42..12050
NAME/KEY: primer bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42..12603
NAME/KEY: primer bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41..15012
NAME/KEY: primer bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41..15482
NAME/KEY: primer bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841..15012
NAME/KEY: primer bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841..15012
NAME/KEY: primer bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842..15012
NAME/KEY: primer bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842..15012
NAME/KEY: primer bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853..15012
NAME/KEY: primer bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853..15012
NAME/KEY: primer bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis complement

OTHER INFORMATION: 17-42-319.mis complement
 NAME/KEY: primer_bind
 LOCATION: 15222..15240
 OTHER INFORMATION: 17-41-250.mis
 NAME/KEY: primer_bind
 LOCATION: 15242..15260
 OTHER INFORMATION: 17-41-250.mis complement
 NAME/KEY: primer_bind
 LOCATION: 42199..42217
 OTHER INFORMATION: 20-841-149.mis
 NAME/KEY: primer_bind
 LOCATION: 42219..42237
 OTHER INFORMATION: 20-841-149.mis complement
 NAME/KEY: primer_bind
 LOCATION: 45433..45441
 OTHER INFORMATION: 20-842-115.mis
 NAME/KEY: primer_bind
 LOCATION: 45433..45461
 OTHER INFORMATION: 20-842-115.mis complement
 NAME/KEY: primer_bind
 LOCATION: 77059..77057
 OTHER INFORMATION: 20-853-415.mis
 NAME/KEY: primer_bind
 LOCATION: 77059..77077
 OTHER INFORMATION: 20-853-415.mis complement
 NAME/KEY: misc_binding
 LOCATION: 1227..1251
 OTHER INFORMATION: 20-828-311.probe
 NAME/KEY: misc_binding
 LOCATION: 12335..12359
 OTHER INFORMATION: 17-42-319.probe
 NAME/KEY: misc_binding
 LOCATION: 15229..15553
 OTHER INFORMATION: 17-41-250.probe
 NAME/KEY: misc_binding
 LOCATION: 2206..42230
 OTHER INFORMATION: 20-841-149.probe
 NAME/KEY: misc_binding
 LOCATION: 45435..45454
 OTHER INFORMATION: 20-842-115.probe
 NAME/KEY: misc_binding
 LOCATION: 77046..77070
 OTHER INFORMATION: 20-853-415.probe
 US-09-750-580-1

OTHER INFORMATION: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 6517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 8025
 LENGTH: 195
 TYPE: DNA
 ORGANISM: *Drosophila melanogaster*
 US-09-270-767-8025

Query Match 2.2%; Score 38.2; DB 4; Length 195;
 Best Local Similarity 52.1%; Pred. No. 0.31; Mismatches 0; Indels 0; Gaps 0;
 Matches 85; Conservative 0; MisMatches 78; Indels 0; Gaps 0;

Qy 7 GATAATAAGTAAGTCAGAAATAATAATTCCAAATTTTTAATAGACCA 66
 Db 33 GATCGTAACACATCACAAATAAAGAACACTCACTCATATTGGGCTAACCA 92

Qy 67 GTGCCAACAGTACAAAGTAAAACCTCAAAATTCCCTATTATGGACTTATATTG 126
 Db 93 ATTATATCAACAAATAAACCAAATAACAGTGTAAAAGTAGTAAAGGTGTTA 152

127 GACGGAGGAGTAGAGATGTAGCCAGAAACAAAAAC 169
 Db 153 AAAACAGATTAAATAATGAAATAAAACAAAAAC 195

RESULT 13
 US-09-270-767-23307
 Sequence 23307, Application US/09270767
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 23307
 ; LENGTH: 195
 ; TYPE: DNA
 ; ORGANISM: *Drosophila melanogaster*
 US-09-270-767-23307

Query Match 2.2%; Score 38.2; DB 4; Length 195;
 Best Local Similarity 52.1%; Pred. No. 0.31; Mismatches 0; Indels 0; Gaps 0;
 Matches 85; Conservative 0; MisMatches 78; Indels 0; Gaps 0;

Qy 7 GATAATAAGTAAGTCAGAAATAATAATTCCAAATTTTTAATAGACCA 66
 Db 33 GATCGTAACACATCACAAATAAAGAACACTCACTCATATTGGGCTAACCA 92

Qy 67 GTGCCAACAGTACAAAGTAAAACCTCAAAATTCCCTATTATGGACTTATATTG 126
 Db 93 ATTATATCAACAAATAAACCAAATAACAGTGTAAAAGTAGTAAAGGTGTTA 152

127 GACGGAGGAGTAGAGATGTAGCCAGAAACAAAAAC 169
 Db 153 AAAACAGATTAAATAATGAAATAAAACAAAAAC 195

RESULT 14
 US-09-806-708B-22/C
 Sequence 22, Application US/09806708B
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of British Columbia
 ; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
 ; FILE REFERENCE: 4810-58741
 ; CURRENT APPLICATION NUMBER: US/09/806,708B
 ; CURRENT FILING DATE: 2001-04-03

RESULT 12
 US-09-270-767-8025
 Sequence 8025, Application US/09270767
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*



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OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 13:10:01 ; Search time 901 Seconds

Perfect score: 10627.326 Million cell updates/sec
(without alignments)

Title: US-10-009-570-1

Sequence: 1 acttttagataataaaatgttaag,.....ctcttctcccttcagtgcagg 1772

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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20: /cgn2_6/_ptodata/2/_pubpna/_us60_new_pub.seq:*

21: /cgn2_6/_ptodata/2/_pubpna/_us60_pubcomb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
C 1	134.4	7.6	187	17	US-10-437-963-100861
C 2	87.8	5.0	2000	16	US-10-260-238-1841
C 3	85.8	4.8	5579	16	Sequence 100861, Sequence 1841, Ap
C 4	84.2	4.8	2000	16	Sequence 1, Appli
C 5	80.4	4.5	12120	10	Sequence 2087, Ap
C 6	80	4.5	2000	16	Sequence 19, Appli
C 7	78	4.4	2000	16	Sequence 215, Ap
C 8	76.8	4.3	1912	16	Sequence 2454, Ap
C 9	76.8	4.3	2000	16	Sequence 1722, Ap
C 10	75	4.2	6064	17	Sequence 1664, Ap
C 11	73.8	4.2	2000	16	Sequence 10006, Ap
C 12	73.4	4.1	5216	17	Sequence 2176, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
US-10-437-963-100861/c
i Sequence 100861, Application US/104379963
i Publication No. US20040123334A1
i GENERAL INFORMATION:
i APPLICANT: La Rosa, Thomas J.
i APPLICANT: Kovalic, David R.
i APPLICANT: Zhou, Yihua
i APPLICANT: Cao, Yongwei
i APPLICANT: Wu, Wei
i APPLICANT: Boukarov, Andrey A.
i APPLICANT: Barbozuk, Brad
i APPLICANT: Li, Ping

i TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
i Title of Invention: Plants and Uses Thereof For Plant Improvement
i FILE REFERENCE: 38-21(5322)B
i CURRENT APPLICATION NUMBER: US/10/437,963
i CURRENT FILING DATE: 2003-05-14
i NUMBER OF SEQ ID NOS: 204966
i SEQ ID NO 100861
i LENGTH: 187
i TYPE: DNA
i ORGANISM: Oryza sativa
i FEATURE:
i OTHER INFORMATION: Clone ID: PAT_MRT4530_98536C.1
i US-10-437-963-100861

Query Match 7.6%; Score 134.4; DB 17; Length 187;
Best Local Similarity 85.6%; Pred. No. 1.1e-23; N mismatches 0; Indels 26; Gaps 1;

Matches 161; Conservative 0; N mismatches 26; Indels 1; Gaps 1;
Qy 190 GGATGATCTAGTCGGACATTTGAGGTCTGCGACATGGCTACACAC 249
Db 187 GGATGATCTAGTCGGCTATTGAGTGGCAATTGAGTGGCTGACGC 128

RESULT 2

Qy 250 TGCCTCTTCAGTGCTAGCTGATGTTCTGTCATATTACATGGCAGGAGCTA 309
Db 127 TG-TTCTTCAGTAAGCCAACTGCAAGTGTGTTCTGCAATGCAAGCTA 69

Qy 310 GCAACAGTTGCGGAAACATCGATAATCATTGTTGCAAGGGAAACATGGGAAAC 369
Db 68 GCGACAGTTGCGGAACTGTCAGTCAGTGTGTCAGTGTGCACTGAGCTAAAGC 9

Qy 370 CGGGGTG 377
Db 8 CGGGGTG 1

RESULT 3

Qy 1 Sequence 1, Application US/10168273B
; Publication No. US20040058124A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Masahiro
; TITLE OF INVENTION: PLANT LESION FORMATION SUPPRESSING GENE, Sp17 AND USE THEREOF
; FILE REFERENCE: 23572-005 NATL
; CURRENT APPLICATION NUMBER: US/10/168, 273B
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/JP01/09153
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: JP 2000-318557
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 5579
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: genomic DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3711)..(3947)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4185)..(5327)
; US-10-168-273B-1

Query Match 4.8% Score 85.8; DB 16; Length 5579;
Best Local Similarity 88.2%; Pred. No. 1.3e-10;
Matches 105; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

Qy 1 ACTTTAGATAAAAGTAAGTCAAGCAAGAAATAATAATATTCCAAATTTTTATAA 60
Db 2257 ACTTTAGATAAAAGTAAGT -CAAAAGATAATAATAATTTTATAA 2314

Qy 61 AGACGACTGGTAAAGTACAGTACAGTAAACTCAAAATCTTATAATTATGGACTTAT 119
Db 2315 AGACGATGGTCAACAGTGCATAAAACTCAAGTCCCTTATAATTATGGATAAT 2373

RESULT 4

Qy 1 Sequence 2087, Application US/10260238
; Publication No. US2004016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provert, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260, 238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325, 448
; PRIOR FILING DATE: 2001-09-16
; PRIOR APPLICATION NUMBER: US 60/325, 277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370, 620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO: 1841
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: N region
; LOCATION: (661)..(661)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (682)..(683)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (749)..(749)
; OTHER INFORMATION: n = any nucleotide
; US-10-260-2087-1841

Query Match 5.0% Score 87.8; DB 16; Length 2000;
Best Local Similarity 85.2%; Pred. No. 2.4e-11;
Matches 98; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 ACTTTAGATAAAAGTAAGTCAAGAAATAATAATTCCAAATTTTTATAA 60
Db 1825 ACTTTGGATAAAAGCAAGTCAAAATAATAATTCAATTTTATAA 1884

Qy 61 AGACGAGTGGTCAACAGTACAGTAAACTCAAAATCTTATAATTATGGAC 115
Db 1885 AGACGAAATGATAAAAGTATATACAAATCCCTTATAATTAGAGAC 1939

RESULT 3

Qy 1 Sequence 1, Application US/10168273B
; Publication No. US20040058124A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Masahiro
; TITLE OF INVENTION: PLANT LESION FORMATION SUPPRESSING GENE, Sp17 AND USE THEREOF
; FILE REFERENCE: 23572-005 NATL
; CURRENT APPLICATION NUMBER: US/10/168, 273B
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/JP01/09153
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: JP 2000-318557
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 6077
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2087
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa

FEATURE:
 NAME/KEY: N region
 LOCATION: (433)..(433)
 OTHER INFORMATION: n = any nucleotide

FEATURE:
 NAME/KEY: N region
 LOCATION: (1346)..(1346)
 OTHER INFORMATION: n = any nucleotide

FEATURE:
 NAME/KEY: N region
 LOCATION: (1355)..(1355)
 OTHER INFORMATION: n = any nucleotide

FEATURE:
 NAME/KEY: N region
 LOCATION: (1386)..(1386)
 OTHER INFORMATION: n = any nucleotide

FEATURE:
 NAME/KEY: N region
 LOCATION: (1394)..(1394)
 OTHER INFORMATION: n = any nucleotide

FEATURE:
 NAME/KEY: N region
 LOCATION: (1402)..(1402)
 OTHER INFORMATION: n = any nucleotide

US-10-260-238-2087

Query Match 4.8%; Score 84.2; DB 16; Length 2000;
 Best Local Similarity 88.0%; Pred. No. 2e-10;
 Matches 103; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

Qy 3 TTAGATATAAGTAAGTCAAGAAGAAATAATAATTCAAATTTTTAATAG 62
 Db 344 TTGGGATAATAAGTAAGTCAAGAAGAAATAATAATTCAAATTTTTAATAG 286

Qy 63 ACAGTGTCAACAGTCAAGTAAACTAAATACTAAATTGGACTTAT 119
 Db 285 ATGAGTGTCAACAGTGTCAAGCAAAACTAAATACTAAATTGGACGGAT 229

RESULT 5
 US -09-840-743-19/C
 ; Sequence 19, Application US/09840743
 ; Publication No. US20030135890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer, Robert L.
 ; APPLICANT: Choi, Yeonhee
 ; APPLICANT: Hannan, Mike
 ; APPLICANT: Okamura, Jack Kishiro
 ; APPLICANT: Tatarinova, Tatiana Valerievna
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Nucleic Acids That Control Plant Development
 ; FILE REFERENCE: 023070-099910US
 ; CURRENT APPLICATION NUMBER: US/09/840,743
 ; CURRENT FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: US 09/553,690
 ; PRIOR FILING DATE: 2000-04-21
 ; NUMBER OF SEQ ID NOS: 119
 ; SOFTWARE: PatentIn Ver. 2.1
 ; LENGTH: 12120

Query Match 4.5%; Score 80.4; DB 10; Length 12120;
 Best Local Similarity 73.4%; Pred. No. 4.6e-09;
 Matches 116; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

Qy 1 ACTTTAGATATAAGTAAGTCAAGAAGAAATAATAATTCCAAATTTTTAAAT 59
 Db 11342 ACTGTGAAATAAGTAAGTCAAGAAGAAATAATAATTCCAAATTTTTAAAT 11283

RESULT 6
 US-10-260-238-2150
 ; Sequence 2150, Application US/10260238
 ; Publication No. US20040016025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd G.
 ; APPLICANT: Moughamer, Todd G.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katajiri, Fumiyaki
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Provar, Nicholas
 ; APPLICANT: Ricks, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-NP
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO: 2150
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 US-10-260-238-2150

Query Match 4.5%; Score 80; DB 16; Length 2000;
 Best Local Similarity 86.2%; Pred. No. 2.3e-09;
 Matches 100; Conservative 15; Indels 1; Gaps 1;

Qy 1 ACTTTAGATATAAGTAAGTCAAGAAGAAATAATAATTCCAAATTTTTAAAT 59
 Db 352 ACGGTAGATATAAGTAGTTACAATAATAATAATTCCAAATTTTTGAAAT 411

Qy 60 AAGACGAGTGTCAAACAGTCAAGTAAACTCAAATTCCCTTATATTGGAC 115
 Db 412 AAGACGAGTGTCAAATGTGAAACAAATCAAAATCCCTTATATTGGAC 467

RESULT 7
 US-10-260-238-2454
 ; Sequence 2454, Application US/10260238
 ; Publication No. US20040016025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd G.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katajiri, Fumiyaki
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Provar, Nicholas
 ; APPLICANT: Ricks, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-NP
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO: 2454
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: DMTRICE sequence from PAC P0489609
 US-09-840-743-19

Query Match 4.5%; Score 80.4; DB 10; Length 12120;
 Best Local Similarity 73.4%; Pred. No. 4.6e-09;
 Matches 116; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

Qy 1 ACTTTAGATATAAGTAAGTCAAGAAGAAATAATAATTCCAAATTTTTAAAT 59
 Db 11342 ACTGTGAAATAAGTAAGTCAAGAAGAAATAATAATTCCAAATTTTTAAAT 11283

FILE REFERENCE: 60111-NP
 CURRENT APPLICATION NUMBER: US/10/260,238
 PRIORITY NUMBER: US 2002-09-26
 PRIORITY NUMBER: US 60/325,448
 PRIORITY NUMBER: US 2001-09-26
 PRIORITY NUMBER: US 60/325,277
 PRIORITY NUMBER: US 60/370,620
 SEQ ID NO: 24/4
 LENGTH: 2000
 TYPE: DNA
 ORGANISM: *Oryza sativa*

FEATURE:
 NAME/KEY: N_region
 LOCATION: (705)..(705)
 OTHER INFORMATION: n = any nucleotide

US-10-260-238-2454

Query Match 4.4%; Score 78; DB 16; Length 2000;
 Best Local Similarity 85.2%; Pred. No. 7.3e-09;
 Matches 98; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy 1 ACTTTAGATAAAAGTAAGTCACAGAAAATAATAATTCAGAAATTTTATAA 60
 Db 677 ACTTGGATAAAAGTAATCACATATAATAATAATTTTTTTATAA 736

Qy 61 AGACGAGGTGTCAACAGTCAAGTAAAGAAAACTCCTTATATGGGA 114
 Db 737 AGACGATTTGTCAACAGTGTCAAAAGTCATAATCCCTTATATAGGA 791

RESULT 8
 US-10-260-238-1722/C
 Publication No. US/0040016025A1

GENERAL INFORMATION:
 APPLICANT: Budworth, Paul R.
 APPLICANT: Moughamer, Todd G.
 APPLICANT: Briggs, Steven P.
 APPLICANT: Cooper, Bret
 APPLICANT: Glazebrook, Jane
 APPLICANT: Goff, Stephen A.
 APPLICANT: Katagiri, Fumiyoiki
 APPLICANT: Kreps, JoeL
 APPLICANT: Provert, Nicholas
 APPLICANT: Rikke, Darrell
 APPLICANT: Zhu, Tong

TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 CURRENT APPLICATION NUMBER: US/10/260,238
 CURRENT FILING DATE: 2002-09-26
 PRIORITY NUMBER: US 60/325,448
 PRIORITY NUMBER: US 2001-09-26
 PRIORITY NUMBER: US 60/325,277
 PRIORITY NUMBER: US 60/370,620
 SEQ ID NO: 1722
 LENGTH: 1912
 TYPE: DNA
 ORGANISM: *Oryza sativa*

US-10-260-238-1722

Qy 60 AAGAGGAGTGTCAAACAGTACAGACTAAATTTCTTATATGGGAC 115
 Db 1507 AAGAGGAGTGTCAAACAGTACAGACTAAATTTCTTATATGGGAC 1452

RESULT 9
 US-10-260-238-1664/C
 Publication No. US/0040016025A1

GENERAL INFORMATION:
 APPLICANT: Budworth, Paul R.
 APPLICANT: Moughamer, Todd G.
 APPLICANT: Briggs, Steven P.
 APPLICANT: Cooper, Bret
 APPLICANT: Glazebrook, Jane
 APPLICANT: Goff, Stephen A.
 APPLICANT: Katagiri, Fumiyoiki
 APPLICANT: Kreps, JoeL
 APPLICANT: Provert, Nicholas
 APPLICANT: Rikke, Darrell
 APPLICANT: Zhu, Tong

TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 CURRENT APPLICATION NUMBER: US/10/260,238
 CURRENT FILING DATE: 2002-09-26
 PRIORITY NUMBER: US 60/325,448
 PRIORITY NUMBER: US 2001-09-26
 PRIORITY NUMBER: US 60/325,277
 PRIORITY NUMBER: US 60/370,620
 SEQ ID NO: 6077
 LENGTH: 1664

Query Match 4.3%; Score 76.8; DB 16; Length 2000;
 Best Local Similarity 84.5%; Pred. No. 1.5e-08;
 Matches 98; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Qy 1 ACTTTAGATAAAAGTAAGTCACAGAAAATAATAATTCAGAAATTTTTTT AAT 59
 Db 1161 ACTTGGATAAAAGTAAGTCACAAATAATAATTTAAAAAATTAAAT 1102

Qy 60 AAGAGGAGTGTCAAACAGTACAGACTAAATTTCTTATATGGGAC 115
 Db 1101 AAGAGGAGTGTCAAACAGTACAGACTAAATTTCTTATATGGGAC 1046

RESULT 10
 US-10-437-963-10006
 Publication No. US/10437963

GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovacic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Bookharov, Andrey A.
 APPLICANT: Babazuk, Brd
 APPLICANT: Li, Ping

TITLE OF INVENTION: Plant Nucleic Acid Molecules and Other Molecules Associated With
 Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO: 10006
 LENGTH: 6064

Qy 1 ACTTTAGATAAAAGTAAGTCACAGAAAATAATAATTCAGAAATT-TTTTAAAT 59
 Db 1567 ACTATAGATAAAAGTAAGTCACAGAAAATAATAATTCAGAAATT 1508

TYPE: DNA
 FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT450_16369C.1

Query Match 4.2%; Score 75; DB 17; Length 6064;
 Best Local Similarity 88.9%; Pred. No. 7.5e-08;
 Matches 104; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

Qy 1 ACTTTAGATAATAAGTAAAGTCAAGAGAAAAATAATAATTCCAAATTTTT-AA 58
 Db 3210 ACTTGGATATAAGCAGTCGA-AAAATAATAATAATTCAAAATTGGAA 3268

Qy 59 TAAGACGAGTGGTCAAAACTCAAGTAAACTCAAAATTCCCTTATATTGGAC 115
 Db 3269 TAAGACGAGTAAATCAGTCAAAACTCAAAATTCCCTTATATTGGAC 3325

RESULT 11
 US-10-260-238-2176
 Sequence 2176, Application US/10260238
 Publication No. US20040016025A1
 GENERAL INFORMATION:
 APPLICANT: Budworth, Paul R.
 APPLICANT: Moughamer, Todd G.
 APPLICANT: Briggs, Steven P.
 APPLICANT: Cooper, Bret
 APPLICANT: Glazebrook, Jane
 APPLICANT: Goff, Stephen A.
 APPLICANT: Katagiri, Fumiaki
 APPLICANT: Kreps, Joe
 APPLICANT: Provert, Nicholas
 APPLICANT: Ricke, Darrell
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 FILE REFERENCE: 60111-NP
 CURRENT APPLICATION NUMBER: US/10/260,238
 CURRENT FILING DATE: 2002-09-26
 PRIOR APPLICATION NUMBER: US 60/325,448
 PRIOR FILING DATE: 2001-09-16
 PRIOR APPLICATION NUMBER: US 60/325,277
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: US 60/370,620
 PRIOR FILING DATE: 2002-04-04
 NUMBER OF SEQ ID NOS: 6077
 SEQ ID NO 2176
 LENGTH: 2000
 TYPE: DNA
 ORGANISM: Oryza sativa
 FEATURE:
 NAME/KEY: N region
 LOCATION: (573)..(573)
 OTHER INFORMATION: n = any nucleotide
 FEATURE:
 NAME/KEY: N region
 LOCATION: (600)..(600)
 OTHER INFORMATION: n = any nucleotide
 FEATURE:
 NAME/KEY: N region
 LOCATION: (1711)..(1711)
 OTHER INFORMATION: n = any nucleotide
 FEATURE:
 NAME/KEY: N region
 LOCATION: (1941)..(1941)
 OTHER INFORMATION: n = any nucleotide
 FEATURE:
 NAME/KEY: N region
 LOCATION: (1960)..(1960)

OTHER INFORMATION: n = any nucleotide
 FEATURE:
 NAME/KEY: N region
 LOCATION: (1968)..(1968)
 OTHER INFORMATION: n = any nucleotide
 FEATURE:
 NAME/KEY: N region
 LOCATION: (1991)..(1991)
 OTHER INFORMATION: n = any nucleotide
 FEATURE:
 NAME/KEY: N region
 LOCATION: (1994)..(1994)
 OTHER INFORMATION: n = any nucleotide
 FEATURE:
 NAME/KEY: N region
 LOCATION: (1999)..(1999)
 OTHER INFORMATION: n = any nucleotide
 US-10-260-238-2176

Query Match 4.2%; Score 73.8; DB 16; Length 2000;
 Best Local Similarity 84.1%; Pred. No. 8.5e-08;
 Matches 95; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Qy 1 ACTTTAGATAATAAGTAAAGTCAAGAGAAAAATAATAATTCCAAATTTTT-AAT 59
 Db 1551 ACCTGATATAAGTAAAGTAACTCAAAATAATTCCAAAATTGGAT 1610

Qy 60 AAGACGAGTGGTCAAAACTCAAGTAAACTCAAAATTCCCTTATATTGG 112
 Db 1611 AATACGAGTGTCAAACCTGTAAGTAAACCTCAAAATCCCTTATATTGG 1663

RESULT 12
 US-10-437-963-50400/C
 Sequence 50400, Application US/10437963
 Publication No. US200412334A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovacic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbuzuk, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5322)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 50400
 LENGTH: 5216
 TYPE: DNA
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_52890C.1
 US-10-437-963-50400

Query Match 4.1%; Score 73.4; DB 17; Length 5216;
 Best Local Similarity 84.7%; Pred. No. 1.8e-07;
 Matches 94; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy 1 ACTTTAGATAATAAGTAAAGTCAAGAGAAAAATAATAATTCCAAATTTTT-AAT 59
 Db 5074 ACTTTAGATAATAAGTCAAGTAACTCAAAATAATTCAAAATTAAAT 5015

Qy 60 AAGACGAGTGGTCAAACTACATACAGTAAACACTCAAACTCAAAATCCCTTATATT 110
 Db 5014 AAGACAACTGTTGCAAACTGTTGCAACACTACAGTAAACACTCAAAATCCCTTATATT 4964

RESULT 13

US-10-260-238-1731/C
 Sequence 1731, Application US/10260238
 Publication No. US20040016025A1
 GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd G.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiaki
 ; APPLICANT: Krepp, Joe
 ; APPLICANT: Provert, Nicholas
 ; APPLICANT: Ricker, Darrell
 ; APPLICANT: Zhu, Tong
 TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 FILE REFERENCE: 601111-NP
 CURRENT APPLICATION NUMBER: US/10/260,238
 CURRENT FILING DATE: 2002-09-26
 PRIORITY APPLICATION NUMBER: US 60/325,448
 PRIORITY FILING DATE: 2001-09-26
 PRIORITY APPLICATION NUMBER: US 60/325,277
 PRIORITY FILING DATE: 2001-09-26
 PRIORITY APPLICATION NUMBER: US 60/370,620
 PRIORITY FILING DATE: 2002-04-04
 NUMBER OF SEQ ID NOS: 6077
 SEQ ID NO 1731
 LENGTH: 2000
 TYPE: DNA
 ORGANISM: *Oryza sativa*
 US-10-260-238-1731

Query Match 4.1%; Score 72.8; DB 16; Length 2000;
 Best Local Similarity 80.8%; Pred. No. 1.5e-07; Mismatches 0; Indels 1; Gaps 1;
 Matches 97; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

Qy 1 ACTTTAGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 60
 Db 1119 ACTTTGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 1061

Query Match 6.1%; Score 61.0; DB 17; Length 1480;
 Best Local Similarity 85.5%; Pred. No. 1.2e-06; Mismatches 0; Indels 15; Gaps 2;
 Matches 100; Conservative 15; Indels 2; Gaps 2;

Qy 1 ACTTTAGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 59
 Db 1287 ATTTAGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 1228

Query Match 4.1%; Score 72.2; DB 17; Length 2955;
 Best Local Similarity 83.2%; Pred. No. 2.6e-07; Mismatches 0; Indels 1; Gaps 1;
 Matches 94; Conservative 18; Mismatches 1; Indels 1;

Qy 1 ACTTTAGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 60
 Db 2919 ACTCTGGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 2861

Query Match 6.1%; Score 61.0; DB 17; Length 1480;
 Best Local Similarity 85.5%; Pred. No. 1.2e-06; Mismatches 0; Indels 15; Gaps 2;
 Matches 100; Conservative 15; Indels 2; Gaps 2;

Qy 1 ACTAGAGT-GGTCAACAGTACAGTAAACTCAAATTTCTTATATGGAC 115
 Db 1227 AGAGGAGTGGTCAAACCTAACAGCAAAACTAAATCCTTATATGGAC 1171

Search completed: November 17, 2004, 16:37:15
 Job time : 903 secS

RESULT 14
 US-10-437-963-34025/C
 Sequence 34025, Application US/10437963
 Publication No. US20040123343A1
 GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 34025
 LENGTH: 2955
 TYPE: DNA
 ORGANISM: *Oryza sativa*
 FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_38080C.1

Qy 60 AGAGGAGT-GGTCAACAGTACAGTAAACTCAAATTTCTTATATGGAC 115
 Db 1227 AGAGGAGTGGTCAAACCTAACAGCAAAACTAAATCCTTATATGGAC 1171

Query Match 4.1%; Score 72.2; DB 17; Length 2955;
 Best Local Similarity 83.2%; Pred. No. 2.6e-07; Mismatches 0; Indels 1; Gaps 1;
 Matches 94; Conservative 18; Mismatches 1; Indels 1;

Qy 1 ACTTTAGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 60
 Db 2919 ACTCTGGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 2861

Query Match 6.1%; Score 61.0; DB 17; Length 1480;
 Best Local Similarity 85.5%; Pred. No. 1.2e-06; Mismatches 0; Indels 15; Gaps 2;
 Matches 100; Conservative 15; Indels 2; Gaps 2;

Qy 1 ACTTTAGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 59
 Db 1287 ATTTAGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 1228

Query Match 4.1%; Score 72.2; DB 17; Length 2955;
 Best Local Similarity 83.2%; Pred. No. 2.6e-07; Mismatches 0; Indels 1; Gaps 1;
 Matches 94; Conservative 18; Mismatches 1; Indels 1;

Qy 1 ACTTTAGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 60
 Db 2919 ACTCTGGATAATAAGTAAGTCACAGAAAAATAATAATTCCAATTTTATA 2861

Query Match 6.1%; Score 61.0; DB 17; Length 1480;
 Best Local Similarity 85.5%; Pred. No. 1.2e-06; Mismatches 0; Indels 15; Gaps 2;
 Matches 100; Conservative 15; Indels 2; Gaps 2;

Qy 1 ACTAGAGT-GGTCAACAGTACAGTAAACTCAAATTTCTTATATGGAC 115
 Db 1227 AGAGGAGTGGTCAAACCTAACAGCAAACTAAATCCTTATATGGAC 1171

Search completed: November 17, 2004, 16:37:15
 Job time : 903 secS

RESULT 14
 US-10-437-963-34025/C
 Sequence 34025, Application US/10437963
 Publication No. US20040123343A1
 GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 34025
 LENGTH: 2955
 TYPE: DNA
 ORGANISM: *Oryza sativa*
 FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_38080C.1

Qy 60 AGAGGAGT-GGTCAACAGTACAGTAAACTCAAATTTCTTATATGGAC 115
 Db 1227 AGAGGAGTGGTCAAACCTAACAGCAAACTAAATCCTTATATGGAC 1171

Result No.	Score	Query Match	Length	DB ID	Description	Source
C 1	460.6	26.0	493	9 AB157032	AB157032 Oriza sativa	1. /organism="Oriza sativa (japonica cultivar-group)"
C 2	148.2	8.4	626	9 CL552633	CL552633 OR_BBA009	/clone_xref="T27150T"
C 3	131.4	7.4	802	9 CL549942	CL549942 OR_BBA008	/clone_lib="PCR product directly amplified from rice genomic DNA"
C 4	99	5.6	609	9 CL709885	CL709885 OR_BBA003	/note="The 3' end of retrotranspon Tos17 was found immediately upstream of this sequence."
C 5	98.2	5.5	663	8 AQ872280	AQ872280 nbep0047D	
C 6	97.2	5.5	783	9 CL734947	CL734947 OR_BBA006	
C 7	95.8	5.4	681	9 CL837854	CL837854 OR_BBA006	
C 8	92.6	5.2	406	9 CL712255	CL712255 OR_BBA003	
C 9	92.6	5.2	641	9 CL625050	CL625050 OR_BBA002	
C 10	91	5.1	703	9 CL725327	CL725327 OR_BBA005	
C 11	90.4	5.1	582	9 CL788096	CL788096 OR_BBA010	
C 12	90.4	5.1	660	9 CL826141	CL826141 OR_BBA004	
C 13	90.2	5.1	764	9 CL795980	CL795980 OR_BBA000	
C 14	89.4	5.0	881	9 CL732336	CL732336 OR_BBA006	
C 15	88	5.0	566	9 CL617540	CL617540 OR_BBA001	
C 16	88	5.0	569	8 AQ272200	AQ272200 nbxb0027L	
C 17	88	5.0	643	9 CL770798	CL770798 OR_BBA014	
C 18	88	5.0	767	9 CL732306	CL732306 OR_BBA006	
C 19	87.8	5.0	375	9 CL788567	CL788567 OR_BBA009	
C 20	87.8	5.0	482	9 CL520455	CL520455 SAKIGOB9	
C 21	87.8	5.0	573	9 CL743078	CL743078 OR_BBA007	
C 22	87.8	5.0	820	8 AQ861700	AQ861700 nbxb0017G	
C 23	87	4.9	478	9 CL733727	CL733727 OR_BBA006	
C 24	87	4.9	680	8 AQ289268	AQ289268 nbxb0034B	

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OM nucleic - nucleic search, using SW model

Run on: November 17, 2004, 10:45:20 ; Search time 5094 Seconds (without alignments)

12675.933 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 actttagataataaaatggtaaag.....ctcttccttcgtgcgaag 1772

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen Parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hrc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_ges1:*

9: gb_ges2:*

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hrc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_ges1:*

9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

RESULT 1	
LOCUS	AB157032/c
DEFINITION	Oriza sativa (japonica cultivar-group) DNA, clone:T27150T, 3', flanking sequence of Tos17 insertion in rice strain NG0531, genomic survey sequence.
ACCESSION	AB157032
VERSION	AB157032.1 GI:40315745
KEYWORDS	GSS.
SOURCE	Oriza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
ORGANISM	
REFERENCE	Miyao,A., Tanaka,K., Murata,K., Sawaki,H., Takeda,S., Abe,K., Shinozuka,Y., Onosato,K. and Hirochika,H.
AUTHORS	
TITLE	Target site specificity of the Tos17 retrotransposon shows a preference for insertion within genes and against insertion in retrotransposon-rich regions of the genome
JOURNAL	Plant Cell 15 (8), 1771-1780 (2003)
PUBLMED	12897251
REFERENCE	1. Miyao,A. and Hirochika,H.
AUTHORS	
TITLE	Submitted (19-DEC-2003) Akio Miyao, National Institute of Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp), URL:http://tos.nias'affrc.go.jp/, Tel:81-298-38-7020, Fax:81-298-38-7020, Location/Qualifiers
FEATURES	1. .493
Source	/organism="Oriza sativa (japonica cultivar-group)" /clone_xref="T27150T" /clone_lib="PCR product directly amplified from rice genomic DNA" /note="The 3' end of retrotranspon Tos17 was found immediately upstream of this sequence."

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Source
C 1	460.6	26.0	493	9 AB157032	AB157032 Oriza sativa	1. /organism="Oriza sativa (japonica cultivar-group)"
C 2	148.2	8.4	626	9 CL552633	CL552633 OR_BBA009	/clone_xref="T27150T"
C 3	131.4	7.4	802	9 CL549942	CL549942 OR_BBA008	/clone_lib="PCR product directly amplified from rice genomic DNA"
C 4	99	5.6	609	9 CL709885	CL709885 OR_BBA003	/note="The 3' end of retrotranspon Tos17 was found immediately upstream of this sequence."
C 5	98.2	5.5	663	8 AQ872280	AQ872280 nbep0047D	
C 6	97.2	5.5	783	9 CL734947	CL734947 OR_BBA006	
C 7	95.8	5.4	681	9 CL837854	CL837854 OR_BBA006	
C 8	92.6	5.2	406	9 CL712255	CL712255 OR_BBA003	
C 9	92.6	5.2	641	9 CL625050	CL625050 OR_BBA002	
C 10	91	5.1	703	9 CL725327	CL725327 OR_BBA005	
C 11	90.4	5.1	582	9 CL788096	CL788096 OR_BBA010	
C 12	90.4	5.1	660	9 CL826141	CL826141 OR_BBA004	
C 13	90.2	5.1	764	9 CL795980	CL795980 OR_BBA000	
C 14	89.4	5.0	881	9 CL732336	CL732336 OR_BBA006	
C 15	88	5.0	566	9 CL617540	CL617540 OR_BBA001	
C 16	88	5.0	569	8 AQ272200	AQ272200 nbxb0027L	
C 17	88	5.0	643	9 CL770798	CL770798 OR_BBA014	
C 18	88	5.0	767	9 CL732306	CL732306 OR_BBA006	
C 19	87.8	5.0	375	9 CL788567	CL788567 OR_BBA009	
C 20	87.8	5.0	482	9 CL520455	CL520455 SAKIGOB9	
C 21	87.8	5.0	573	9 CL743078	CL743078 OR_BBA007	
C 22	87.8	5.0	820	8 AQ861700	AQ861700 nbxb0017G	
C 23	87	4.9	478	9 CL733727	CL733727 OR_BBA006	
C 24	87	4.9	680	8 AQ289268	AQ289268 nbxb0034B	

Query Match 26.0% Best Local Similarity 98.4%; Score 460.6; DB 9; Length 493; Matches 485; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

FEATURES	source	Query Match Best Local Similarity Matches	Score 131.4; Pred. No. 6.1e-22; Conservative 0; Mismatches 116;	DB 9; Length 802;	FEATURES	source	Query Match Best Local Similarity Matches	Score 99; Pred. No. 9e-14; Conservative 0; Mismatches 10;	DB 9; Length 609;
		QY	196	CATCTTGGTGGCACATTGAGGGTGGCGTAGAGGAGTACCTCTACAACTGCTTC		QY	1	ACTTTAGATAATAAAGTAACTAAGTCACAGAAANATAATAATATTCCAAATTTTTTATA	
		Db	515	CATCTGGCCGCAC-CGGAGAGTGGCGCAGA---GTGACCTTAACAGCTGCTTC		Db	455	ATTTTGGATAAAAGTAAAGTCACAGAAANATAATAATTTAAATTTTATA	
		QY	256	TTCAGTGGTAGCTGATGCTGATGTTCTGCATTACATTCAGGGAGCAGCTGAAACA		QY	61	AGACGGAGTGGTAAACAGTAAAGTAAACTCAGAAATACTCCTTATAATTATGGAC	
		Db	460	TTCACTGAG-AAGGAAAGCTGATGCTCTGAT---TTCAGGAGCACTAGGACCA		Db	515	AGACGATGGTAAACAGTAAATTAAACTCAGAAATACTCCTTATAATTATGGAC	
		QY	316	GTTCAGGAGACAATCGATAATCCATTGTCAGGGAGAACATGGAGAAAACGGGGC					
		Db	406	GTTCATGGGACAGTGCACAACTGTCAGGAGAACATGAGAAAACGGGGCG					
		QY	376	TGGAGAGAAAGGGAGCAGCGTACCGTACCTTCTGAAGCTGACCCATCTGGAAT					
		Db	346	GAGACGAAACAAACAGGGTACAGTGAACCTTCTGGAGCTGAAACCCGGCGCAAT					
		QY	436	CGCGAGATTGGTTGTCAATT---CCAACTTGCAGTCCTCTCAGATTGGTG-----					
		Db	286	CGCGAGATTGGTTGTCCAGGGTCTAGTGGAGTCCTCTCAGATTGGTGATGATC		RESULT 5	AQ872280	663 bp	DNA
		QY	485	---CATGTTAACCTA - GTACATCTGAAATAATGAAG-TGTAAATACCTTGAGAAGA		LOCUS	AQ872280	663 bp	DNA
		Db	226	TGACATCTTCACACTTACCGTACATGAAATGTTGAAATAATCTCTAAAGA		DEFINITION	rheb0047D09r	CUGI Rice BAC Library (B20R)	linear
		QY	538	CCTCATGGAACTGTCAGTCGCTGAGGATTAGCTAAGAAAAAAATAATGACTTTC		KEYWORDS	riceb0047D09r	Orzya sativa (japonica cultivar-group)	GSS
		Db	166	CCGTATGTAAGAATGCTGTCATGAACTTACCGTATATTGCTATTTGGAAATTA		ORGANISM		Orzya sativa (japonica cultivar-group)	
		QY	598	GAAACTTAATTGGAGTATTAGATTAGTTAGGTT 632		ACCESSION	AQ872280	Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Liliopsida; Poaceae; Bhrhartoidea; Orzyeae; Orzya.	
		Db	106	AACTAAACTTAAATTCTATAGTTGATTCTGTGT 72		VERSION	AQ872280.1	GI:6222731	
RESULT 4	CL709985	CL709985	609 bp	DNA	REFERENCE	Wing, R.A. and Dean, R.A.			
LOCUS		DEFINITION	OR_BBA0033C05.r OR_BBA	OR	AUTHORS				
DEFINITION		3', genomic survey sequence.	Orzya rufipogon genomic clone	OR_BBA0033C05	TITLE				
ACCESSION		CL709985			JOURNAL				
VERSION		CL709985			COMMENT				
KEYWORDS		CL709985.1			Unpublished (1998)				
SOURCE		GSS.			Contact: Wing, R.A.				
ORGANISM		Orzya rufipogon			Clemson University Genomics Institute				
		Oryza rufipogon			100 Jordan Hall, Clemson, SC 29634, USA				
		Spermatophyta; Magnoliophyta; Liliopsida; Poaceae;			Te: 864 656 7288				
		Ehrhartoidea; Orzyeae; Orzya.			Fax: 864 656 4293				
					Email: rwing@clemson.edu				
					Seq Primer: GGAAACAGCTATGACCATG				
					Class: BAC ends				
					High quality sequence start: 47				
					High quality sequence stop: 343.				

FEATURES	source	LOCUS	DEFINITION	COMMENT
Location/Qualifiers		CL734947	CL734947 OR_BBa006BF07.f OR_BBa Oryza rufipogon genomic clone OR_BBa006BF07	783 bp DNA linear GSS 27-JUL-2004
1 .663 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="genomic DNA" /cultivar="Nipponbare" /clone="nbel004/D09r" /tissue_type="Leaf" /lab_host="E. coli DH10B" /clone_lib="CUGI Rice BAC Library (EcoRI)" /note="Vector: pBACIndigo; Site 1: EcoRI; Site 2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from <i>Oryza sativa</i> , Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,236 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation of a particular sequence with a probability of 99.9%. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."	CL734947 OR_BBa006BF07.f OR_BBa Oryza rufipogon genomic clone OR_BBa006BF07			
FEATURES	source	CL837854	CL837854 OR_CBa0063G17.r OR_CBa Oryza rufipogon genomic clone OR_CBa0063G17	681 bp DNA linear GSS 09-AUG-2004
ORIGIN		LOCUS	DEFINITION	
Query Match 5.5% ; Score 98.2 ; DB 8 ; Length 653 ; Best Local Similarity 89.1% ; Pred. No. 1.5e-13 ; Mismatches 0 ; Indels 0 ; Gaps 0 ; Matches 105 ; Conservative 0 ; N mismatches 13 ; Indels 0 ; Gaps 0 ;	CL837854 OR_CBa0063G17.r OR_CBa Oryza rufipogon genomic clone OR_CBa0063G17			
QY 1 ACTTTAGATAATAAGTAACTCAGAAATAATAATTCCAAATTTTATAA 60	QY 1 ACTTTAGATAATAAGTAACTCAGAAATAATAATTCCAAATTTTATAA 60	ORGANISM	Organism	
Db 200 ACTTTGGATAATAAGTAACTCAGAAATAATAATTCCAAATTTTATAA 259	Db 200 ACTTTGGATAATAAGTAACTCAGAAATAATAATTCCAAATTTTATAA 259	DEFINITION	Oryza rufipogon	
QY 61 AGACAGGTGGTCAACAGTACAAAGTAAACTCAGAAATAATTCCAAATTCTTATATTGGGACTTAT 119	QY 61 AGACAGGTGGTCAACAGTACAAAGTAAACTCAGAAATAATTCCAAATTCTTATATTGGGACTTAT 119	COMMENT	Oryza rufipogon	
Db 260 AGACAGGTGGTCAACAGTCAAGCTTAAGCTAAACTCAGAAATAATTCCAAATTCTTATATTGGAGCGAT 318	Db 260 AGACAGGTGGTCAACAGTCAAGCTTAAGCTAAACTCAGAAATAATTCCAAATTCTTATATTGGAGCGAT 318	ACCESSION	Oryza rufipogon	
ORIGIN		CL837854	CL837854 OR_CBa0063G17.r OR_CBa Oryza rufipogon genomic clone OR_CBa0063G17	
Query Match 5.5% ; Score 98.2 ; DB 8 ; Length 653 ; Best Local Similarity 89.1% ; Pred. No. 1.5e-13 ; Mismatches 0 ; Indels 0 ; Gaps 0 ; Matches 105 ; Conservative 0 ; N mismatches 13 ; Indels 0 ; Gaps 0 ;	QY 1 ACTTTAGATAATAAGTAACTCAGAAATAATAATTCCAAATTTTATAA 60	DEFINITION	Oryza rufipogon	
Db 200 ACTTTGGATAATAAGTAACTCAGAAATAATAATTCCAAATTTTATAA 259	Db 200 ACTTTGGATAATAAGTAACTCAGAAATAATAATTCCAAATTTTATAA 259	COMMENT	Oryza rufipogon	
QY 61 AGACAGGTGGTCAACAGTACAAAGTAAACTCAGAAATAATTCCAAATTCTTATATTGGGACTTAT 119	QY 61 AGACAGGTGGTCAACAGTACAAAGTAAACTCAGAAATAATTCCAAATTCTTATATTGGGACTTAT 119	ACCESSION	Oryza rufipogon	
Db 260 AGACAGGTGGTCAACAGTCAAGCTTAAGCTAAACTCAGAAATAATTCCAAATTCTTATATTGGAGCGAT 318	Db 260 AGACAGGTGGTCAACAGTCAAGCTTAAGCTAAACTCAGAAATAATTCCAAATTCTTATATTGGAGCGAT 318	KEYWORDS	Oryza rufipogon	
RESULT 6	source	CL734947	CL734947 OR_BBa006BF07.f OR_BBa Oryza rufipogon genomic clone OR_BBa006BF07	783 bp DNA linear GSS 27-JUL-2004
LOCUS		LOCUS	DEFINITION	
DEFINITION OR_BBa006BF07.f OR_BBa Oryza rufipogon genomic clone OR_BBa006BF07	CL734947	CL734947 OR_BBa006BF07.f OR_BBa Oryza rufipogon genomic clone OR_BBa006BF07	5' , genomic survey sequence.	
COMMENT		CL734947	CL734947 OR_BBa006BF07.f OR_BBa Oryza rufipogon genomic clone OR_BBa006BF07	5' , genomic survey sequence.
ACCESSION CL734947		ACCESSION CL734947	DEFINITION	
VERSION 1		VERSION 1	DEFINITION	
KEYWORDS 1 (bases 1 to 783)		KEYWORDS 1 (bases 1 to 783)	DEFINITION	
SOURCE GSS		SOURCE GSS	DEFINITION	
ORGANISM Oryza rufipogon		ORGANISM Oryza rufipogon	DEFINITION	
COMMENT		COMMENT	DEFINITION	
REFERENCE 1 (bases 1 to 783)		REFERENCE 1 (bases 1 to 783)	DEFINITION	
AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and Wing,R.		AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and Wing,R.	DEFINITION	
JOURNAL OMAP Project		JOURNAL OMAP Project	DEFINITION	
COMMENT Unpublished (2004)		COMMENT Unpublished (2004)	DEFINITION	
FORWARD: TAA TAC GAC TCA CTA TAG GG		FORWARD: TAA TAC GAC TCA CTA TAG GG	DEFINITION	
BACKWARD: CAC TCA TTA GGC ACC CCA		BACKWARD: CAC TCA TTA GGC ACC CCA	DEFINITION	
PLATE: 0063		PLATE: 0063	PLATE: 0063	
ROW: G		ROW: G	ROW: G	
COLUMN: 17		COLUMN: 17	COLUMN: 17	
SEQ PRIMER: CAC TCA TTA GGC ACC CCA		SEQ PRIMER: CAC TCA TTA GGC ACC CCA	SEQ PRIMER: CAC TCA TTA GGC ACC CCA	
CLASS: BAC ends		CLASS: BAC ends	CLASS: BAC ends	
LOCATION/QUALIFIERS		LOCATION/QUALIFIERS	LOCATION/QUALIFIERS	
1. .681 /organism="Oryza rufipogon"		1. .681 /organism="Oryza rufipogon"	LOCATION/QUALIFIERS	
/mol_type="genomic DNA"		/mol_type="genomic DNA"	1. .681 /organism="Oryza rufipogon"	
/db_xref="taxon:4529"		/db_xref="taxon:4529"	/mol_type="genomic DNA"	
/clone="OR_CBa006BF07"		/clone="OR_CBa006BF07"	/db_xref="taxon:4529"	
/tissue_type="young leaves"		/tissue_type="young leaves"	/clone="OR_CBa006BF07"	
/lab_host="DH10B T1 phage resistant"		/lab_host="DH10B T1 phage resistant"	/tissue_type="young leaves"	
/clone_id="OR_CBa"		/clone_id="OR_CBa"	/lab_host="DH10B T1 phage resistant"	
/note="Vector: pAGIBAC1"		/note="Vector: pAGIBAC1"	/clone_id="OR_CBa"	
PCR PRIMERS		PCR PRIMERS	/note="Vector: pAGIBAC1"	
FORWARD: TAA TAC GAC TCA CTA TAG GG		FORWARD: TAA TAC GAC TCA CTA TAG GG	PCR PRIMERS	

"Firik treated 36 hrs before harvest"

TITLE OMAP Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: <http://genome.arizona.edu>
PCR PRIMERS
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 **Std Error**: 0.00
Plate: 0055 **row**: D **column**: 11
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
FEATURES
source Location/Qualifiers
 1. .703
 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_BBa0055D11"
tissue type="young leaves"
 /lab host="OR_BBa"
 /clone lib="OR_BBa"
 /note="Vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII"
RIGIN
 Query Match 5.1†; Score 91; DB 9; Length 703;
 Best Local Similarity 87.0%; Pred. No. 9.7e-12;
 Matches 100; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 1 ACTTTAGATAATAAGTAGTCAAGAAATAATAATTCCAAATTTTTAAATA 60
 657 ACTTTGATATAATAAGTAGTCAAGAAATAATAATTCCAAATTTTTCAATA 598
 61 AGRCGAGSTGGTCAAACAGCTACAGTAAACACTCAAATTCTTATTATTGGAC 115
 597 AGRCGAAATGTTAAACAGTCAAGTCAAATAACCTCTTATTATAGAAC 543
RESULT 11
 CL788096/c CL788096 582 bp DNA linear GSS 30-JUL-2004
LOCUS OR_BBa0106H03.f OR_BBa Oryza rufipogon genomic clone OR_BBa0106H03
DEFINITION 5', genomic survey sequence.
ACCESSION CL788096
VERSION CL788096.1 GI:50867747
KEYWORDS GSS.
ORGANISM Oryza rufipogon
 Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
 Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 582)
AUTHORS Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R., R.
 Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
TITLE OMAP Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
PCR PRIMERS
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 **Std Error**: 0.00
Plate: 0106 **row**: H **column**: 03
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.

FEATURES	Location/Qualifiers
source	<p>1. .582</p> <p>/organism="Oryza rufipogon"</p> <p>/mol_type="genomic DNA"</p> <p>/db_xref="taxon:4229"</p> <p>/clone="OR_CBA010B03"</p> <p>/tissue_type="young leaves"</p> <p>/lab_host="DH10B-T1 phage resistant"</p> <p>/clone_idb="OR_BBA"</p> <p>/note="vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII</p>
ORIGIN	<p>Query Match Score 90.4; DB 9; Length 582;</p> <p>Best Local Similarity 75.7%; Pred. No. 1.3e-11;</p> <p>Matches 112; Conservative 0; Mismatches 0; Gaps 0;</p> <p>Qy 1 ACTTACATAAAAGTAAGTCACTACAGAAATAATAAATTCATAAATTTATAA 60</p> <p>Db 315 ACTGCGATAATAAGTAAGTCACATAATAATAATAATTTATAAATTTGATA 256</p> <p>Qy 61 AGACAGTGGTCAAACAGTACAAGTAAAGTCAAATTCCTTATTATGGACTTATA 120</p> <p>Db 255 AGACAGTGGTCAAACGTTGAAACGTTGAAACAAACTTAAATCTTATATTCTGGCGATG 196</p> <p>Qy 121 TTATGGACGGAGGAGTAGAGATGTT 148</p> <p>Db 195 GAGTGTAGTGTAGTAGTGTAGTGTAGTGT 168</p>
RESULT 1.2	
LOCUS	CL826141/c 660 bp DNA linear GSS 09-AUG-2009
DEFINITION	OR_CBA010B09.r OR_CBA Oryza rufipogon genomic clone OR_CBA0016L09
ACCESSION	3', generic survey sequence.
VERSION	CL826141
KEYWORDS	CL826141.1 GI:51071751
SOURCE	GSS.
ORGANISM	Oryza rufipogon
SPECIES	Oryza rufipogon
PHYLUM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CLASS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
ORDER	Elatinidae; Poales; Oryzeae; Oryzae.
REFERENCE	1 (bases 1 to 660)
AUTHORS	Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
TITLE	OMAP project
JOURNAL	Unpublished (2004)
COMMENT	Contact: Rod A. Wing
	Arizona Genomics Institute
	University of Arizona
	Forbes Building Room 303, Tucson, AZ 85721-0036, USA
	Tel: 520 626 9595
	Fax: 520 621 1259
	Email: http://genome.arizona.edu
FEATURES	<p>PCR Primers</p> <p>FORWARD: TAA TAC GAC TCA CTA TAG GG</p> <p>BACKWARD: CAC TCA TTA CGC ACC CCA</p> <p>Plate: 0046 row: 1 column: 09</p> <p>Seq primer: CAC TCA TTA CGC ACC CCA</p> <p>Class: BAC ends.</p>
source	<p>1. .660</p> <p>/organism="Oryza rufipogon"</p> <p>/mol_type="genomic DNA"</p> <p>/db_xref="taxon:4529"</p> <p>/clone="OR_CBA0046L09"</p> <p>/tissue_type="young leaves"</p> <p>/dev_stage="week old seedlings"</p> <p>/lab_host="DH10B-T1 phage resistant"</p> <p>/clone_idb="OR_CBA"</p> <p>/note="vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII</p> <p>drk treated 36 hrs before harvest"</p>

ORIGIN

Query Match 5.1%; Score 90.4; DB 9; Length 660;
Best Local Similarity 75.7%; Pred. No. 1.e-11;
Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 ACTTGTATATAAGTAGTCAAGAAAATAATAATTCCAAATTTTATAA 60
Db 329 ACTGTGATATAAGTAGTCAAGAAAATAATAATTCCAAATTTTATAA 270

Qy 61 AGACGAGTGGTCAAACACTACAGTAAACTCAAATTCCCTTATATGGAC 115
Db 269 AGATGAGTGGTCAAACACTACAGTAAACTCAAATTCCCTTATATGGAC 120

Qy 121 TTATGGACGAGGAACTAGAAGATTGT 148
Db 209 GAGTGTAGTGTAGTAGTGTAGTGTGT 182

RESULT 13

LOCUS CL795980/c 764 bp DNA linear GSS 06-AUG-2004
DEFINITION 5'- genomic survey sequence.
CL795980

ACCESSION CL795980.1 GI:51017996

VERSION GSS

KEYWORDS Oryza rufipogon

ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Poaceae;

REFERENCE Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudina,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

AUTHORS Unpublished (2004)

TITLE JOURNAL
COMMENT Unpublished (2004)

FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
PCR PRIMERS Insert Length: 161 Std Error: 0.00
Plate: 0065 row: D column: 13
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.

FEATURES Location/Qualifiers

1. . 881
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BBa0065D13"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lab="OR_BBa"
/note="Vector: PAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 5.0%; Score 89.4; DB 9; Length 881;
Best Local Similarity 86.1%; Pred. No. 2.5e-11;
Matches 99; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ACTTGTATATAAGTAGTCAAGAAAATAATAATTCCAAATTTTATAA 60
Db 614 ACTGTAGATATAAGTAGTCAAGAAAATAATAATTCCAAATTTTATAA 673

Qy 61 AGACGAGTGGTCAAACACTACAGTAAACTCAAATTCCCTTATATGGAC 115
Db 674 AGACGAGTGGTCAAACGTACAAAGAAAATAATAATTCCAAATTTTATAA 728

RESULT 15

LOCUS CL617540/c 566 bp DNA linear GSS 01-JUL-2004
DEFINITION OR_BBa010K04.r OR BBa Oryza rufipogon genomic clone OR_BBa010K04
3'- genomic survey sequence.

ACCESSION CL617540

VERSION GSS

KEYWORDS Oryza rufipogon

SOURCE Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

ORGANISM

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 566)

REFERENCE Kim.H., Yu.Y., Stum.D., Yost.D., Rao.K., Luo.M., Jetty.R.,
AUTHORS Kudrna.D., Muller.C., Hatfield.J., Soderlund.C. and Wing.R.,
TITLE OMAP Project
JOURNAL Unpublished (2004)

COMMENT Contact: Rod A. Wing

Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: <http://genome.arizona.edu>

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG

BACKWARD: CAC TCA TTA GGC ACC CCA

Insert Length: 161

Std Error: 0.00

Plate: 0010 row: K column: 04

Seq primer: CAC TCA TTA GGC ACC CCA

Class: BAC ends.

FEATURES Location/Qualifiers

1. .566

/organism="Oryza rufipogon"

/mol_type="genomic DNA"

/db_xref="taxon:529"

/clone="OR_BRA0010K04"

/tissue_type="young leaves"

/lab_host="DB110B-T1 phage resistant"

/clone_lib="OR_BBa"

/note="vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match Score 88; DB 9; Length 566;
Best Local Similarity 90.5%; Pred. No. 5.4e-11;
Matches 105; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ACTTTAGATAAAGTAACTAAGTCACAGAAATAATAATTCAAATTTTTAAAT 59

Db 530 ACTTTGGATAAAGTAAGTCACAGAAATAATAATTCAAATTTTTAAAT 471

Qy 60 AAGACGAGTGTCAAACAGTACAAGTAAAGTCAAATTCCTTATATATGGGAC 115

Db 470 AAGACGAAATGTCAAACAGTCAAAGTCAAAGTCAAATCCCTTATATGGGAC 415

Search completed: November 17, 2004, 14:35:00
Job time : 5098 secs